

FIGURE 1

GGCTGAGGGGAGGCCGGAGCCTTCTGGGCCCTGGGGATCCTCTGACTGGTGGCTGGA
GAGAACGCCCTGCAGCCAACCAGGTCAAGGTCTGCTCACAGTCTCTCTGGCCGATGTAA
AGGCTTCCACAAAGGAGTGGGAGTCTAACATGAGGCTCTGCAGGCGCTGAGGATGACCC
CAAGCCCTGGACCTGCCGAGCTGGCACTGAGGCAGGGCTGACGCTACTGTGAGGGAAAGA
AGGTTGTGAGCAGCCCCGAGGCCCTGGCAAGCTGGCCAGGCTTGAGGCTCTGCCGGAGCCCT
CTGGAGGAGCAGGGAGCAGCTGGAGGCCCTAGGGCAGGGCTCTGGCAGGCCAGGGCTGCA
ACTCAGAACCCCTCTCAGGGCCATGGACAGGCTGCCCTGAGCAGGCCAGGGTGAAGCATG
TGAGGAGGCCCGAGGAGCAAGCAGGGAGGAAAGGGCTTCATAGATTCTATTCAAAAGA
ATAACCCACATTTCGAAGGACC**AT**GAGGCCACTGTGCTGTGACATGCTGTTGGCTGGACT
CTGGTGGCATGGAGCTGGTGCAGGCCAGGGAGCTTGGAGGACTGAGGAGGGGCTC
GCAAGAGAGTCTTACCTAACAGGTACAAGGGCGGGAGCTTCCAGGACAAGTGTCA
CCTACACCTCATTGTGCCCAAGCAGGGTCACGGGTGCACTGCTCAACTCAAGGAG
CTGGAGGTCTTCTGGAGAACCCAGTGCATAAGCAGAGCTAGACCTGCTCAACATGAGCT
GCTCAAGCAGAACGGCGAGATCGAGACGGCTGAGCAGCTGGTGGAGGTGGAGGGCT
TGAGCAGCTGAAGCTGCTGCCAAGGAGACGCCAATGAACTCCGGCTCACCGACTC
TACATGCAGCTCTGCAGAGATCATCCGAAGCGGACAACGCTGTTGGAGCTTCCAGCT
GGAGAACAGGATCTGAGAACAGCAGCAGACACTGCTGGCAGACAGTCAAGGAC
CTGGAGCACAGTACCCAGCACCTGGCCAATCTGGGCCAACCATGAGATCATCGGCC
CTTGAGGACACTGCCAGGGTGGCCCTCGGCCAGGGCGTCCCCCAGCCACCCCCCTG
CCCCGCCCCGGTCTACCAACACCCACCTACAACCGCATCATCAACCCAGATCTTACCAACG
AGATCCAGAGTGGCAGGACACTGGAGGTGCTGGCACCCCTCTGGCCACTATGCCACTCT
AACCGCCTCCATCTCCAGGACAAGGGCTGGGCCATTGGAGAGACTGCTGCGAGGCC
GGAGGATGCCACGACACCAAGCTCCATACCTGGTAAGCGGAGAACACCAACCGCTCA
TCGAGGTCTGGTGGCAGAGACACGACGCCGGGGCTGGACCTCATCGAGGACGCC
GATGGCTCTGTTAACCTTCTCAGGAACTGGAGACGTCAAGCAAGGGTTGGAAATTG
CGCGAACATACTGGCTGGCCCTGAGAACATTACTGGCTGAGCAACCAAGGAACTACAAAC
TCTGGTGGACCATGGAGGACTGGTCCGGCCCAAAGTCTTGCAGAATACCCAGTTCCG
CTGGAACTCTGAGAGCGATTATAAGCTGGCCTGGGGCTGACCATGGCAATCGGGTGA
CTCTTCTACATGGCAACAGGCAAGCAGTCTACCCACCTGGACAGAGATCATGATGCT
CAGGAAACTGTGCCCACTACCAAGAGGGAGGCTGGTGTATAACCGCTGTGCCACTCAAAC
CTCAACGGGGTCTGGTACCGCGGGGCCATTACCGGAGCCGCTACCAAGGACGGAGCTACTG
GGCTGAGTTCGGAGGGAGGCTTACTACTCAAGAAACTGGTGTATGATGCCAGGACA
CCACACCTTCCACT**TA**GGCAGCTCCCCCTCTGGACCTCTGGCCATTGGCAGGAGGCC
CCCTGGTCAGCTGGCCACAGCAAAAGAACAACTCTCACCAAGTTCATCTGGAGGCTGGG
GAGACGGGGATGCTGGATTCTGTTTCCGAAGTCACTCAGCAGGGATGATGGAACTGAATCGAT
ACGGTGTTCCTGCTCCCTACTTCTTCAACACAGACAGGCCCTCATGTCAGGACA
GGACAGACTACAGACAACCTTCTTAAATAAAATTAGTCTACATAAAATTTA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLAAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLLENRHKQELELLNNELLKQKRIETLQLVEVDGGIVSEVKLLR
KESRNMNSRVTQLYQMLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSILPSSTDKPGPWRDCLQALEDGHDTSSIYLVKpentNRLMQVWCQDR
HDPPGGWTVIQRRLDGSVNFFRNWETYKQGFGNIDGEYWLGLENIYWLTNQGNYKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHVDYTGNCAYHQ
KGGWWYNACAHSNLNGWYRGGHYRSRYQDGVYWAERGGSYSLKKVMMIRPNPNTFH

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Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471, 473-479

Amidation site.

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

FIGURE 3

FIGURE 4

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846
<subunit 1 of 1, 117 aa, 1 stop
<MW: 12692, pI: 7.50, NX(S/T): 0
MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPIRRGRGPHEPRRKQNVVDGLVLDTLAVIRTLVDK
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Important features:

Signal peptide:

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

CCCACGGTCCGGCAGTCGGCAGTTCTGCCCTGCCAGTCGCCCGATCCGG
 CCCGGGCTGTGGCTGACTCGGACCCAGGCAGCAGCCCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCTTGCTGAAGCCGAGTGCAGGAGA
 GCCCGGCAAACGAGCTAAAGGAGACCAAAGCGCGAAGTCGAGACAGCGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGCGAACCCAGAGAGGGCAGCAAAGAAGCGTGGTGGTGGG
 CGTCGTGCCATGGCGCGGCTATGCCAGCTCGCTATCGTCAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCGCTGCAAGTGTGTCAGCAGCCCGAGCAAAGGCAAGACAGCTGC
 GACAAAAACAAAGTTAAATGTTTCCGGGTCAAACCTTCGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGGGATGGAACCATTTGATGGCACCAAAGATGAGGAGACGACTTACACT
 CTGTTAACCTCATCCCTGTGGGCTGCGAGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTGGCAATGAAACAGTGAGGGTACTTGTACACTCGGAACCTTACACACTGAGTGCA
 AATTCAAAGAATCAGTGGAAAATTATTATGTGACATATTCAATGATATACCGTCAG
 CAGCAGTCAGGGAGGGTGGTATCTGGGCTGAAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAGCCTGCAGCTCATTTCGCTAAACCAACTGAAAGTGGCATGT
 ACAAGGAGCCATCACTGCACGGATCTCACGGAGTTCTCCCGATCTGGAAAGCGGGACCCAAACC
 AAGAGCAGAAGTGTCTGGCGTGTGAAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
 GTTAGCCAGTGAAGGCAAAGGGCTGTAAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTCACCCAAAGTCAAATTGTCAGTGACATTACCAAAACACAGG
 CAGAGTTCACTATTCTATGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSACKCVSSPSKGKTCDKNKLNVFSRVKLFGSKKRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGKDEDSTYTLFNLI PVGLRVVAI QGVQTKLYLA
MNSEGYYLTSELFTEPKFKEFESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGHNVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 7

ATGGCCGGGCCATCGCTAGGGCTTGATCCGCCAGAGCGGCAGGCCGGAGCAGCACTG
 GGACCGGCCGTCTGCCAGCAGGAGGGAGCAGCCCAGCAAGAACCGCGGGCTCTGCAACG
 GCAACCTGGTGGATATCTCTCAAAGTGCATCTCGGCCTCAAGAACGCGAGGTTGC
 CGCCAAGATCCCCAGCTCAAGGTATAGTGACCAGGTTATATTGCAAGGCTACTACT
 GCAAATGCACCCCGATGGAGCTCGATGAAACCAAGGATGACAGCACTAATTCTACACT
 TCAACCTCATACCAGTGGGACTACGTGTTGCCATCCAGGGAGTGA
 AAAACAGGGTTGTAT
 ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
 TAAAGAATCTGTTTGAAATTATTATGTAATCTACTCATCCATGTTGACAGACAA
 CAGG
 AATCTGGTAGAGCCTGGTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAA
 CAGA
 GTAAAGAAAACCAACCCAGCAGCTCATTTCTACCCAGCCATTGGAA
 GTGCCATGTACCG
 AGAACCATCTTGATGATGTTGGGAAACGGTCCCGAAGCCTGGGTGACGCCAAGTAAA
 GCACAAAGTGCCTGCAATAATGAATGGAGGCAACCAAGTC
 AACAGACTAAGACAACAT**TAG**

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKQAREQHWDRPSASRRRSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGIVTRLYC RQGYYLQMHPDGALDGTKD DSTNSTLFNLIPVGLRVVAI QGVKTGLY
IAMN GEGYLYPSELF TPECKF KESV FENYYVIYSSMLYRQQESGR AWFLGLNKEGQAMGNR
VKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSAS AIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 9

CTCGCAGCCGAGCGCGCCGGGAAGGGCTCTCCCTCCAGCGCCGAGCACTGGCCCTGGCA
 GACGCCCAAGATTGTGTAGGAGCTAGCCAGTTGTAGCCCTGAACTGAAACAGCT
 GTGTCCAGACTGAGGCCCAATTGCAATTGTTAACATACTTAGAAAATGAAGTGTCTT
 TAACATTCTCTCCAAATTGGTTAACATACTTAGAAAATGAAGTGTCTT
 GCTTGCCTGAGGGCTCTGCAGTGGCTGGGAGACCCGGCGCTCTCCCTGTCCTCTCA
 CGACTCGCTGGCCCTCTGAAATAAACACCCGGAGCCCCGAGGGCCAGAGGAGGCCGA
 CGTGGCCAGCTCTCGGGGTCGGCGAGCTTCTTCGCTTCGCACTCTCTCC
 TCGCGCTTGGAC**ATCGAGA**ATAAAAGGATACTCACTGTTACATTCTGGCTCTCTG
 TCTTCCAAGCCCTGGGAATGCAACAGGACAGTCAGCAATGCTTGAACCTGGATCGCAGT
 CAGGACAGTGTATTGATGAATGCGAACCATCCCGAGGCCTGCGAGGGAGACATG
 ATGTGTGTTAACAAAACGGGGTATTATGCACTCCCGAGGACAAACCTGTGATGAGG
 GCCCTACTCGAACCCACTCGACCCCTACTCAGGCTCGTACCCAGCAGTGGCCAC
 TCTCAGCTCAAACATACCCACGATCTCAGGCTCTTATATGCCGTTGATACAGATG
 GATGAGAACAACTATGTGGATGAGTGGCAACAGATTCCCACAGTGAAACCC
 CACCCAGATCTGCATCAATACTGAAGGCGGTACACCTGCTCCGACAGCAGGATATTGG
 TTCTGGAAGGCCACTGCTTAGCATGATGATGCTTACTGTTACTGCCAGCAGCTGT
 GCGAATGTTCTGGATCCTATTCTGTACATGCAACCTGGTTTACCTCAATGAGGATGG
 AAGGTCCTGCAAGATGTAACGAGTGTGCCACAGAACCCCTGGCTCAAACTGGCTA
 ACACATTACGGCTCTCATCGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGT
 CATTGCACTGATATGGACGACTGCACTCTCTGAGTTCTCTGCCAACATGAGTGTGAA
 CCAGCCGGCACATACCTCTGCTCCGCTCCAGCTACATCTGCTGGATGACAACCGAA
 GCTGCAAGACATCACAAAGATGTGAGCACAGGAACACAGTCAACCTGCGAGACGTG
 TACAATTACAAGGGGCTTAAATGATCGACCCCATCCGGCTGTGAGGAGCCTTATCTGAG
 GATCACTGATAACCCGCTGTATGTGTCCTGCTGAGAACCTGGCTGAGAGACAGCCCTTA
 CCATCTTGTACCGGGACATGGACGCTGGTCAAGGACCTCCGGCTGACATCTCCAA
 ATGCAACCCACGGCCCTACCCCTGGGCTTATTACATTTCAGATCAAACTGGGATGAA
 GGGCAGAGAATTTCATCGGGCAAACGGGCCCCATCAGTGGCACCCCTGGTGTGACACGCC
 CCATCAAAAGGGGGAAATTCAGCTGGACTGGAAATGATCACTGTAACACTGTCATC
 AACCTCAGGGCAGCTCGTGTACCTGACTGGGATAATGTCAGTACCCATTCT**TGAGC**
 CTCGGCTGGAGCTCCGACCTCTCATGGCACCAGGGACAGAGAGAGGGAAA
 TAACAGAGAGAATGAGAGGCACACAGACGTTAGGCATTCTGCTGAAACGTTCCCGAAGA
 GTCAAGGGCTTCTGACTTCAGCTCACCTGACTATTGCAAGACCTGTCACCCCTGAGGACTTG
 CCACCCCTGGTCTATGACACAGTTTAAAGGTTTATCATGCTCCCTGAGAAGA
 TTGTTGGTAATTTCAGGCTTCAAGGCTTCAAGTTTATTCACATTTCAAAGAAAATGATTAGG
 TTGCGGGGGCTGAGCTATGTTCAAAGACTGTGAAACAGCTGCTGACTTCTCACCT
 TTCAACTCTTCTCTCACTGTTACTGCTTGCAGAACAGGCGGAGCTGGCGGGAAACCC
 GGGAGTAGCTAGTTGTTTGGTACACAGAGAAGGCTATGTAACAAACACAGGAA
 TCGAAGGGTTTTAGAGAATGTTCAAAACCATGCTGGTATTTCACCCCTGAGGACTTG
 TTCACTGTTGCTTAAATTGTTAAACGGTTTAAATTGCTTGTCTGTTCAACCATAAAAGAAG
 AAAAATATGCTGAGAATTCTCGAAAGGCCCTAGACACATGCTATGTCCTTCC
 AAACCCAGTCTCTCCATTAGGCCAGTGTGTTCTTGAGGACCCCTAACTGCTT
 CTTTAGAATTTCACCAATTGGATTGGAATGCAAGAGGCTCCTAAACTGATTAAATTTG
 AGAGA

FIGURE 10

MPGIKRILTVTILALCLPSPGNAQAOCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
 NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNO
 CVDVDECATDSHCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
 SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSЛИCRCDPGYELEEDGVHCSDM
 DECSFSEFLCQHECVNQPGTYFCSCPQGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
 GFKCIDPIRCEEPYLRLISDNRCMCPAENPGCRDQPFITLYRDMDVSGRSVPADIFQMQATT
 RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGS
 SVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 11

CAGGTCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACCGTCCGAAACACAGGTCTTGTGCTGAGAGAACAGTGTGTTGCTG
 GAAGGAGGGAGTGCGCGGGCTGCCCGGGCTCCCTCCCTGCCGCCCTCAGTGGATGGTT
 CCAGGCACCCCTGTCTGGGGCAGGGAGGGCACAGGCTGCACATCGAAGGTTGGGGTGGGACCA
 GGCTGCCCTCGCCCCAGCATCAGTCTCCCTTGGCGCCCTGGCCCTGCAGACTCTCA
 GGGCTAAGGTCTCTGTTGCTTTGGTCCACCTAGAAGAGGCTCCGCTGACTAAAGAGT
 AGCTTGAGGAGGGACCATGAGGAGCTGCATCTGCTCTGGTGGCGCTTCTCTGGGCTG
 GCTCAGGCTGCCCTGAGCCCTGCGACTGTGGGAAAAGTATGCTTCCAGATGCCGACTG
 TGCTACCGCGACCTAGAAATCTGCCGCGCTGGCTTCCCGGCCATGTGACTACACTGAGCC
 TGTCAGGCAACCGGCTGCCAGGTGGCCGGAGGGTGCGCTCAGGGAGGTGCCCTGCTGAG
 TCGCTGTGGTACAGGATCAGGACAGTCCCGCCAGGTGGCCGGAGGCTTGCCCTCTGAG
 CCATCTAAGAGGCTGGACCTCAGCACAATCTCATCTGACTTTGCTGGAGGACACTGC
 ACAACCTCAGTGCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTCATCCCCGC
 GACGCCCTCCCGCAGCGCTCCGTGCTCTGCGCTCGCTGCAACTCAACCCACCGCTTGAACAC
 ATTGGCCGAGGGACCTTACCCCGCTACCGCGCTGTGGGACCTTGCAAGGATCACAGAGAAC
 CCTTCGACTGCACCTGGCGCATCTGTGGCTCAAGGACATGGGCCCTGACACAGGGCTGTCC
 ATCCCGAGCAGGACAACATGCCCTGACCTCACCCATGTGCTAAGGGTACACCGCTGAG
 CGGCCCTGCCGCACTGGCCATCTGCCGCTGACCTCACCCATGTGCTAAGGGTACACCGCTGAG
 ATGGTGGCGAGCTGGCCCTGGCTTGTGCTGGCACTGCTGAGCTGACCTGTGATGTGGACGGCG
 GCCCCTCAGCTTCACTGGCACATCCAGATAACCCAGTGGCATTGTGGAGATCACAGCCCCAA
 CGTGGGCACTGATGGCGCTGCCCTGGCACCCTGTGGCACTCCACGGCGCTTCC
 AGGGCCTTGGCAATGGCAGCCTGCTATCCCCGACTTGGCAAGCTGGAGGAAGGCACTAC
 AGCTGCTGGCCACCAATGAGCTGGCAGTGTGAGGACTCAGTGGACGTGCGACTGGCAC
 GCCCGGTGAGGGTGTGAGGACACACTGGGCGCAGGTTCCATGGCAAAGGGCTTGAGGGAA
 AGGGCTGCTATACGGTGAAACAGGGTGCAGCATGGGGCGAGGACATGTGGTACATC
 ATCTACCTCAGCGCTGTGGGACCCCTGAGGCTGAGCTGCGAGAAGGGGTCTGGGAGCT
 GCCCCCAGGCTGCTCTGCTGGCCAAGGCTCTCTTCTCTTCTCCTACCTCCCT
AGCCCCCAGGCTCCCTAACTCTCCCTTGGCCCTACCAATGCCCTTAAGTGTG
 CAGGGGTCTGGGCTGGCAACTCTGAGGCTGCAATGGGTGACTTCACATTTCCTACCTCT
 CCTCTAATCTCTCTAGAGCACCTGCTATCCCAACTTCTAGACCTGCTCAAACACTGTA
 CTAGGATAGAATTGATCCCCTAACACTGCTGCGGTGCTCATGCTGTAACAGCATG
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 GCCTCAGTGTGGAAATTCAGGGACTGTGACTGTCAGCTGGCAAGGGCCAGGATTGGGGAA
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 GAACTAGACAGTGGCTGGTATGGCTGAGGCTCCCTGGGGCTGCTCAAGCTCCCTGCT
 CCTTGCTGTTTCTGATGATTGGGGCTTCCCTTACCCCTCCCTCAGCTGCAACCTCTAT
 TGTTGGGATCCAGGATGGCCTTCCCTCCCTAAGGCTCCCTGCTGAGACTGAAA
 CCTGGAACTGTGCTCCCTTCTCCCAACTATGCACTGTTGCTGCTCCCTGCAAAGGC
 CAGCCAGCTGGGAGCAGCAGAGAAATAAACAGCATTCTGATGCCAAAAAAA
 AAGGGCGGGCGCAGCTAGACTGACCT

FIGURE 12

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGF PANVTTLSLSANRL
 PGLPEGA FREVPLLQSLWLAHNEIRTVAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL
 QLLKMDSNELTFIPRDAFRSLRALRSQLQNLHNRLHTLAEGTFTPLTALSHLQINENPFDCTC
 GIVWLKTWALTTAVSIPQCDNIACTSPHVLKGTPSLRLLPPLPCSAPSQVQLSYQPSQDGAE
 PGFVLALHCDVDQGPAPQLHWHIPIPSGIVEITSNVGTDGRALPGTPVASSQPRFQAFANG
 SLLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTV
 DNEVQPSGPEDNVVIIYLSRAGNPEAAEVPGQLPPGLLLLGQSLLLFFLTSF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
 334-340, 350-356, 394-400**Amidation site.**

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

20002796111501

FIGURE 13

CCAGGGCGGGAGGGCAGCGCCCAGCGCTAAACGGGAACAGCCCTGGCTAGGGAGCTGC
 AGCGCAGCAGAGTATCGACGGCGCAGGTTGCGTAGGTGCGGACGAGGAGTTTCCCGGC
 AGCGAGGAGGTCTGAGCAGC**ATGGCCGGAGGAGCGCTTCCCTGCCGCCGCTCTGGCT**
 CTGGAGCATCCTCTGTGCCTGCTGGCACTGCGCCGGAGGCCGGCGCCGAGGAGA
 GCCTGTACCTATGGATCGATGCTACCAGCAAGAGACTCATAGGATTTGAAGAAGATATC
 CTGATTGTTCAAGAGGGAAATGGCACCTTACACATGATTTAGAAAAGCGAACAGAG
 AATGCCAGCTATCCTGCAATATCCATTCCATGAATTTACCTGGCAAGCTGCAGGGCAGG
 CAGAATACCTCATGAATTCTGCTTGCCTGGATAAAGGCATATGGCAGATCCA
 ACCGTCAATGTCCTCTGCTGGAACAGTGCCCTACAAGGCATCAGTTGTTCAAGTTGGTT
 CCCATGTCCTGGAAAACAGGATGGGGTGGCAGCATTGAGTGGATGTGATTGTTAGAATT
 CTGAAGGCAACACCATCTCCAAACACCTCAAATGCTATCTCTTAAACATGTCACAA
 GCTGAGTCCCAGGGGTGCCAAATGGAGGCTTTGTAATGAAAGACGCATCTGCAGTG
 TCCTGATGGGTTCCACGGACCTACTGTGAGAAAGCCCTTGTAACCCACGATGTATGAATG
 GTGGACTTGTGTGACTCCTGGTTCTGCATCTGCCACCTGGATTCTATGGAGTGAACGT
 GACAAAGCAAACGTCACCCACCTGCTTAATGGAGGGACCTGTTCTACCTGGAAAATG
 TATTTGCCCTCCAGGACTAGAGGGAGGCAGTGTGAATCAGCAATGCCAACCCCTGTC
 GAAATGGAGGTAATGCATTGGTAAAGCAAATGTAAGTGTCAAAGGTTACAGGGAGAC
 CTCTGTCACCGCTGCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCAA
 CAAATGCCAATGTCAGAAGGTTGGCATGGAAGACACTGCAATAAAGGTACGAAGGCCAGCC
 TCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGCACGCCCTCACTTAAAG
 GCCGAGGAGCGGGATCCACCTGAATCCAATTACATCTGG**TGA**ACTCCGACATCTGAAAC
 GTTTAAGTTACACCAAGTTCATAGCCTTGTAACTCTTACATGTTGAATGTTCAAATAA
 TGTTCACTTAAAGAATACTGGCTGAAATTATTAGCTTCATTATAAATCACTGAGCT
 GATATTACTCTCCTTTAAGTTCTAAGTACGTCAGTGTAGCATGATGGTATAGATTCT
 TGTTCACTGCTTGGCAGACATTATATTATGTCATTGATCAGGTTAAATTTCAGTG
 TGTAGTTGGCAGATATTCAAAATTACAATGCATTGTTGCTGGGGCAGGGAAACAT
 CAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAATTGGATGGTGCAGTTAATGT
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 TTGCTCTTAATTAAACTCTAACATAATATTGACCTTACATTATTCCAGAGATT
 CAGTATTAAAAAAATTACACTGTGTTGAGCATTAAACAATATAATTATCTA
 AACACAATGAAATAGGAATATAATTGTGAACTTTGCTTGAAGCAATATAATA
 ATTGTAACACACAGCTCTACCTAACATAACATTATTACTGTTGATGTATAAAAT
 AAAGGTGCTGCTTGTGTTGGAAAAA

FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAELYFEFLSRLSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDFKANCST
TCFNGGTCFYPGKICCPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPV
EPGCGAHTCHePNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 15

AGAACCTCAGAAATGTGAGTTATTTGGGAATGGCTGTTGAAATGTCCTACGTAAGCCAA
GAGGAGGTCTTGACTIONGGGTCCCAGGGTACCGCAGATCCAGGGACTGGAGCAGCACTAG
CAAGCTCTGGAGGATGAGCCAGGAGTCTGGAATTGAGGCTGAGCCAAAGACCCCAGGGCCGT
CTCAGTCTCATAAAAGGGATCAGGCAAGGAGGAGTTGGGAGAAACCTGAGAAGGGCTGAT
TTGCAGCATCATGATGGGCCTCTCCTGGCCTCTGCTGTGCTCTGGCCTCCCTCTGAGTC
TCCACCTTGGAACTGCCACACGTGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGC
CACAAGCCCCCTCCCTGGACCTGGGTGCGAAGCTATGAAATTCAACAGCTGCTCCCA
GCGGGCTGTGATATTCACTACCAAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAAT
GGGTGCAAAATACATTCTTACTGAAACTCCGAAACAATTGTGACTCAGCTGAATTTC
ATCCGAGGACGCTTGGACCCGCTCTTGGCTCTGAGCCCTCTGGGGAGCCTGCGGAATCTT
TTCTGAAGGCTACATGGACCCGCTGGGAGGAGAGGGTGTTCCTCCCAGAGTTACTTTAAT
AAAGTTGTTCATAGAGTTGAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
AA

FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCCQYSHKPLPWTWRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

100112796 111501

FIGURE 17

GCGAGAACCTTGCACCGCACAACACTGGGGACGATTCTGATTGATTTGGCCTTCGATCCACCCCTCC
 TCCCTTCATGGGACTTGGGACAACAGCTCCCGACCCGCTCGAGCGCTGAGCAGGGCGTATCCAGGAGC
 CAGGACAGCGCCGGAACAGACCCATGGCTCTGGACCCCAAGATCTTAAGTTGCTGCTTCTATCGTCGCGG
 TTCTGCTGGGGTCCGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTCTCCAGCAGACAGTGGCCCA
 CAGCAACAGGGCACAAGCTCAAAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAATATACTGGAGGCTG
 TAACCCGTGACAGAGGGTGTGGATTACACCATGGCTTCAACAAATTGCTTCTGCCCTGCTATGTACAGTT
 GTAAATCAGCTCAACRAAATAAAAGTCTGTACCCAGACAGACACCGTGTCTAGTGTGAAAAGGAGC
 TCCAGGATAAAACCTCCCCTGAGATGGCGAGCTGAGAACAGGGTGTCCAGAGGGATGTCAGGTGAG
 TAATTGATACCCCCGGAGTCAGCATCAACTGCAAAATGATCAGCTGCCAGTCTGACTGGAAAACCCACAG
 CGGAGGAGCAGTGGACACCATCTGGGGAGTCTGGCTCTCCCTACTACCTTATCATCATAGTGTGTTTA
 GTCATATTAGTGTGGTTGGCTTCTATGAGTGGAGAAATGATCTTCTACCTCAAGGGCAGTCTG
 CTCAGGTGGTGGAGGAGTCCCGACGTGTGACAGACTCTTCTCCGGGGGCGGTTATGCTTCAAGGAGTTC
 CTGGGGCGAGGAAATCCGGCAGACAGGACCTGAGACAGATCTCATAGTGTGACTGTAGTGGCAGAGGAGC
 GAATCCAAGGAGTCAGGAGCTGAGCAGACTAACAGGTGTGACTGTAGTGGCAGAGGAGC
 GGAACAGCAGAGCAGAAGCTGGAGGTGTAGAGGAGGAGCTGCTGGTCACTGAATGAGCCTGAGTCCCGTGCACA
 TCAAGCACCTGGATGCCCTGCCAACTCGAACAGACCATGCAAAAGGAAACAAATTGAGGAACTGTC
 GGCCTCCGAAAAGCTCTTTATGAGAAGAGTGGAGGAGCTGCTGAGTGTCTGGCTCTGCTGCTGCTG
 GAAACAGGAGCTCTCCATTTCTCTACAAAGGGAGGAGCCTGGAGAGAAACAGTCCAGTGT
 CCCATGCCCAACAAACTCTACATCCAAATGGGCAGCTTACCATGTCAGACTTGTGTTACGGACTT
 GGAGATTTTTATGAAATACTGGCTGTGATAGAAGAACCCGGAGAAATATATGAGATTCTGGCTCATAGT
 TATACGATTGTGATTAAGGGCTTGTAGGCGCATTCGGGTGCTCATGCTGAACTTGTG
 GCTGAGGGCAGGTGGATTCTGGAGCTGGGGAGTTTGGAGCACGCCATCAACACAGTGGAACTCCATCTCAAT
 TTAAAAGGAAAAAAAGGGTGTGTTAGGAGTGTCTTCTGAGCTTCTCATCATGAGACGTTTCTTCTG
 TTCTTATATGCAAGCTCATCTACTCTGGTGTGTCATTAATGACATTAACAGATGCCGACAGGCC
 AATGCTTGGCTTATAGTTTAACTTACTTACAGGCGGGATATTCTGTATTTCAGTCTGGATA
 TTTTGACTTAATGAGGATTAACAGACTGGCCACTGTGACTCATGAGCATATGGACTTACAGGGGHTC
 GACTTAGGTTTGGCTTAAGGAGTGGATTATGGGGCTACCCCCACCTTAATTAGAGAAAATTTTATG
 CTTACTACTGGCTGTACATCTTCTGGATTCTGGTATTTGTTATGATGTAACATGGAAAACATTG
 GCACTTATTAGGCCTTGTACATGGGTGCGTGGATAACAAATCAGCAGTCAAAATGACTAAAAATATAACTAGT
 GACGGAGGAGAATCTCCCTCTGGGGAGGCACTACTGCTTCTGGAGACTGGCTTCTGGCCGAGACT
 GACCAAGGGTTGATGGCTGGCAGCTCTCAAGGGCAGCTTGTCTTACTGTATTAGGGTATATAGCA
 TATTATATATAAAATATTATATTATTTATTAATGAGTGGATTACATGGCCAGGGATTAGAG
 CTGGTATCTTGGGAAAGCCATGTTCTGGTGTGCTGGAGCAGTCTGGACTGCACTTCTGGACTTGT
 CACAGCAGATGAGGAGCAGTGGAAATTAAGTGTAGCCGGAGACTGCGAGAGCTCTTCAAGGGCATTACA
 GTTGAACGTTAGTGAATCTTGGCCTCATTTGGCTCAAGGGCAGAGCAGGTGTTATCTGCCCGCATCTGCC
 ATGGCATCAAGGGAAAGATGGAGCTGGCTTGGGAAATGCTGTGAAATGTTGCGCAGTGGCATGGATGGG
 CCCCCTCGCTTCTGGGGTCTGTGAACCTGACTCTGGGGAGCTGGCTTCTGGGGAGACTGGCTGAGCTGGTT
 TAGGGTACAGATTCCCTGGTGGAGGCTGGCCCTCTGTAAGCATCTGACTCATCTCAGAGATTAATCT
 TAAACACTGTGACAAACGGGATCTAAATGGCTGACACATTGTCCTGTGTCAGGTTCTGATTATTTTATTAAA
 AACCTCAGTAACTCTTCTGGCTTCTGGAGCAGACTGGGGAGGAGCTGGGGAGGAGGAGGAGGAGGAG
 CGGATATAGTCATTCTAGGGGTTGAGCTTCTCATCTCAAGGATTGTGTTTGTGCTGGACTGGTTG
 GCTGGGACAAGGTTAGAACCTGGCTGAAGTGGCAGATTGATGTTGTCATGGAGTTTAGGAGGGAGT
 GCGCTTCCGGTCTCGCAGCTTCCATCTCCCACTTCCATCTGGCTCCACACCTGCTCCCTGCACTCT
 GATGACACAGGGTGTCTGGCTCTAGCTTGGCTTCTGGGGCTCTGGAGAGATTCTGAGCTGGTT
 CTGAGAGAGGAGGAGCTGGGGAGGAGCTGGGGAGGAGACTGGCTTCAAGGGCTTCTGAGGAGACTGGCTTCAAG
 CTGAGAGAGGAGCTGGGGAGGAGCTGGGGAGGAGCTGGGGAGGAGACTGGCTTCAAGGGCTTCTGAGGAGACTGGCTTCAAG
 ACCAGGCTTATCACTGTTAAAGCTTATTCTTAAACATAAGGCTTCTGACAAACATGAATGAAATTGTTGGGTTT
 GCGCTGGTTGATTTGTTAGGTTGCTTATACCCGGGCAAAATGACACATAACACCTGTTATATGTA
 TACTCATATGTTTATGACCAAAATAATGAAACCTCATRTTAAAAA
 AAAAAA
 AAAAAA
 AAAAAA

FIGURE 18

MGLWGQSVPASSARAGRYPGARTASGTRPWLLDPKILKFVVFIIVAVLLPVRVDSATIPRQD
 EVPQQTVAPQQQRRLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
 QTNKSSCTTRDTCQCEKGSFQDKNSPEMCRTCRTGCPGRMVKSNCPRSDIKCKNESAA
 SSTGKTPAAEETVTIILGMLASPYHYLIIIVVVLVIIIAVVVVVGFSRKKFISYLGICSGGG
 GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAELTGVTVES
 PEEPQRLLEQAEAEGCQRRLLVNVNDADSADISTLDASTLEEGHAKETIQDQLVGSEKL
 FYEEDEAGSATSCL

Important features of the protein:

Transmembrane domains:

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 19

GCGGCACCTGGAAG**ATG**CGCCCATGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGCTTC
 GCCTCCTGTGTGCCTGGTATTGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
 GTCCAGTGTGCTGCCTATAGCATCCGCAGCATCGGGAGAGGCCTGCTCAAAGCTCAGTCC
 CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCATCTGACACCTATGCCTACAGGTTA
 CTCAGCGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG
 AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGCAACTATGTAAGTGGG
 ATGTGACAGCAACACGATGTTTGTATGATGAGGCATAACTCTGGACCGATGACAAAG
 TTTATTCAAGAGTGTGCTCCAAAATCCCTGCTCTCATGGTGACCTATGACGACGGAAGCAC
 AAGACTGAATAACGATGCCAAGAATGCCATAGAACACTTGGAAAGTAAAGAAATCAGGAACA
 TGAAATTCAAGGTCTAGCTGGGTATTATTGCAAGCAAAAGGCTTGGAAACTCCCTCCGAAATT
 CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGCCCTGAGA
 GATCCAGATAGAAGGCTGCATACCCAAAAGAACGAAGC**TGAC**ACTGCAGGCTCTGAGTAAT
 GTGTTCTGTATAAACAAATGCAGCTGAATCGCTCAAGAATCTTATTCTAAATCCAACA
 GCCCATATTGATGAGTATTTGGTTGTTGTAACCAATGAACATTGCTAGTTGTATCA
 AATCTTGGTACGCACTTATTTATACCACTATTTATGAGTGAAGATGTCATTAGCAGGA
 AACTAAAATGAATGGAAATTCTTAAAAA

FIGURE 20

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNGSPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGPWAEIQIEGCIPKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 21

CCGGGGAGGGGAGGGCCCGTCCCAGCCCTCCCCGTCCTCTCCCCGCCCTCCCCGTCCCTG
 GCCGAAGCTCCGTCGGCCCGGGCCGGCTCCGCCCTCACCTCCGGCGCGCTGCCCTC
 TGCCCGGGTTGTCCAAG**ATG**GAGGGCGCTCCACCGGGGTGCGTCGCCCTCCGGCTCTGCTG
 TTCGTGGCGTACCCGCCCTCCGGCTGGCTGACGACGGGCGCCCCCGAGCCGCCGCGCTGTC
 CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACACTACACTGAAAGATGATGGGACATAT
 CTAACACAGCAGGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAATGACTTA
 CCTGTAATAGTGGTGTAAACCGAATAAGCTGTGAGACTTTGATAGTGAAGAATGAAAATCT
 TGAAAATTGGAGGAAAAAGAATTTGGAATTGTCAGTGTAAAGGATTAGTCAGT
 GGCCTATGACATCTGGTTCAGTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
 GATGGAAAACAAGATTGCAAGAAAGGATGTCACTGAAATTGATATTAGTTAGTAAGAACCGGGG
 AGTACTCAGACATTCAAACATACCCCTCCCTTGGAGAAAGCATGCTACTCTATTCTC
 GAGACAGTGACATTATTACCCCTCTAACCTCTCCAAAAAGAAAGTGTAGTTACTG
 CAAACCACTAGCCAGTATCTTACAGGAATGTGGAAACCACGTAGATGAAGATGTTTAC
 TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCATCTTCATATAAGGTAATGTC
 AGTGGATGGAAAAGTTAGAAAAGATCTGTGAGGTTCTGGAGCAACGTTTCCCAGTATT
 TTTCACTTTGAACATCATGGGGTGGATTACAGGAGCAGCTGTGTAATAACCATCTT
 AAAGGTGTTTCCCAGTTCTGAATACAAAGGAATTCTTCAGTGGATAAAGTGGACGTCA
 TACCTGTGACAGCTATCAACTTATCCAGATGGTCCAGAGAAAAGAGCTGAAACCTTGA
 GATAAAACATGTATT**AAA**ACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCCTCC
 AAATTGCCACTTGAATATAATTCTTAAATCGTT

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGLALRLLLVALPASGWLTGAPEPPPLSGAPQDGIRINVTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNNSGVTRISQTLIVKNELENLEEKYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQQKDVTIEDILVKNRGVLRHSNYTLPLEESMLYSISRDSDIL
FTLPLNLSKKESVSSLQTTSQYLIRNVETTVDEDVLPGKLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFSNVFPVFFQFLNIMVVGITGAAVVITILKVFVFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPEKRAENLEDKTCI

Important features of the protein:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCCATGCCGCTCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGG
 CCCTGGCTTGGGCCCTGGCTTCGTGACCTCATGGCTGGGAACCCCGCCCCGGTGGT
 GTTTGCTGGCTCCAGCAGGGCAGGAGGCCACCTGAGCCTGCTCCAGACTGATCTAC
 CGGGGCCAGTGTCTGGCTCCGGCAACATTGACACCGCCGGTCCAACCTCACCCACCCGG
 GGAACAAAGATCAACCTCTCGCTTCTGGGCTTGTCACTGCCCTCCCTGCCAAAGATTCG
 TGCGACGGCTGGAGTGGCCGGGGCAAGGCGTCCGCATGCTGGGGGCCGCCGCGCTG
 CGAGTGGCCGCCGACTGCTCGGGCTCCGGCGCGCTGAGCTGCGGCTCAGACGGCG
 CCACCTACCGCGACAGTGTGCGAGTGCAGCGCCGGCGCTGGCGCCACCCGGACCTGAGC
 GTCATGTACCGGGCCCTGCGCGCAACTCTGTGACACCGTGTGTGCCCGGCCACAGTC
 GTGCGTCGTGGACCAGACGGGAGCGCCACTGCGTGTGTGAGCGGCCCTGCCCTG
 TGCCCTCAGGCCGGGGCAAGGAGCTTGGCAAAACAAACGTCACCTACATCTCCGTG
 CACATGCCAGGCCACCTGCTCTGGGCCCTCATCGCGTGGCCACCGGGAGCTG
 CGCAGGCCACCCCTGAGGAGGCCAGGTGGTGAGTCTGAGAAGAGGAAGAACTTCGT
GAGGCTCAGGACAGGCCCTGGGCTGGTGGCCAGGGCCCCCATATCCCTGTTATTATT
 GCCACAGCAGAGTCAATTATATGCCACGGACACTCCCTAGACCCGGATTGGGACACT
 GGGGATCCAGAAACCTCTGACGATATCTGGAAAGGACTGAGGAAGGGAGGCCCTGGGGC
 GGCTGGTGGTGGGATAGACCTGCGTCCGGACACTGAGCGCTGATTTAGGGCCCTCT
 AGGATGCCCAAGCCCCATACCTAACGACCTATGGCGGGAGGATTCACCTCCGCTCCT
 TGGGATAAACCTTAAATTATTGCTACTATCAAGAGGGCTGGCATTCTCTGCTGTTAATT
 CCTGAAGAGGCATGACTGCTTCTCAGCCCCAACGCTCTAGCTGGTGTACGGAGGGT
 CTAGCCCTGGGTGTAGCGAGGGCTAGCCCTGGGTAGTACGGAGGGTCTAGCCCTGGGTGAG
 TACGGAGGGTCTAGCCCTGGGTAGTACGGAGGGTCTAGCCCTGGGTGATGGAGGATCTAG
 CCTGGGTGAGTATGGGGCTAGCCTGGGTGAGTATGGAGGGCTAGCCCTGGGTGATAG
 GAGGGCTAGCCTGGGTGAGTATGGAGGGTCTAGCCCTGGGTGTTATGGAGGGCTAGCCTG
 GGTGAGTATGGGGCTAGCCTGGGTGAGTACGGAGGGCTAGCTGGTGTGGGG
 CCTCAGAACACTGTGACCTTAGGCCAGCAAGCCAGGCCCTCATGAAGGCCAACAGGCTG
 CACCATCCCTGCCAGCCCCAGAACACTCCAGCTCCCCACTGCCCTGTGTGCCCTTGCCT
 CCTGTGAAGGCCATTAGAGAAATGCCAGTGTGCCCTGGAAAGGGCACGCCCTGTCTCC
 TGACACGGCTGCTGGCTGGCCACAGAACCAACCGCTCTCCCTGCTGTCCACGTAG
 TTCATGAGGCCAACGTGGCGTGGTCTAGACCTGGAGCAGCCAGGGCAGCTCAGAGCAGGGC
 ACTGTGTCCGGCGGAGCCAAGTCACACTCTGGGGAGCTCTGGCGGGGACACGGGCCACTGC
 TCACCCACTGGCCCCAGGGGGTGTAGACGCCAACAGACTCACGCTGACATGGTGTGACATCCGGAGT
 CCTGGAGCGGGTGTCCAGTGGCACCCTAGGTGCTGCTGCCCTCACAGTGGGTTACA
 CCCAGGGCTCTGGTCCCCACACCTGCCCGGCCAGGCCCTGAGACCCAGACTCCAGCC
 AGACACTGCTCACCCACCAATGAGCCGGGGCTGGCAGACCCAGGCCAGGTGCTGGCTTGG
 CCAGTTCTCCACGAGGCTCACCTCCCCCTCATCTGCGTGTGATGCTCAGAAATGCCCTACC
 TGTGCGCTGCTGTAACACAGCTCAGACAGCTATGGGGAGGGACAACACGGAGGATAT
 CCAGCTTCCCCTGGCTGGGTGAGGAATGTGGGGAGCTTGGCCTACCTCCCTCACGCTCC
 CAGCCCCCAGGGCAGTGGCTACCTGTGGTGGCCAGAAAAGTGGCCCTAGGTTGGGTCTA
 CAGGAGGCCCTAGCCAGGCCACCCACCCCTGGGCCCTGCTCACCAAGGAATAAGA
 CTCAAGCCATAAAAAAAA

FIGURE 24

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306
<subunit 1 of 1, 263 aa, 1 stop
<MW: 27663, pI: 6.77, NX(S/T): 2
MRPGAPGPLWPLPWGALAWAVGFVSSMGSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNキンLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCECAPD
CSCLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCEHVVCPRPQSCVVDQ
TGSAHCVVCRRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEENFV
```

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

FIGURE 25

TGCAGAGCTTGTGGAGGCCATGGGGCGCTCGTCGGGAGCTCGTCTCTCGCTGCTGGGGT
 TGTGGCTTGTGCTGCAGCTGCGGATGCCCGAGGGCGCCGAGCTGCGTCTCGCCAGAT
 AAAATCGCGATTATTGGAGCCGAATTGGTGGCACTTCAGCAGCTATTACCTGCGGCAGAA
 ATTTGGGAAAGATGTGAAGATAGACCTGTTGAAAGAGAAGAGGTGGGGGCGGCTGGCTA
 CCATGATGGTGCAGGGCAAGAACATCAGGGCAGGGGTTCTGTCAATCCATCCTTAAATCTG
 CACATGAAACGTTTGTCAAAGACCTGGTCTCTGCTGTTAGGCCTCTGGTGGCCTACT
 GGGGATATATAATGGAGAGACTCTGGTATTGAGGAGAGCACTGGTCATAATTAAACGTGA
 TAAATTAGTTGGCGCTATGGATTCAATCCCTCGTATGCACATGTGGTAGAGGACGTG
 TTAGACAAGTCATGAGGATCTACCGCTACCAGTCATGACTATGCCTCAGTAGTGTGCGA
 AAAATTACTCATGCTCTAGGAGGAGTGAATTCCCTGGAATGCTTAATCGAACACTTCTG
 AAACCTTGCAAAAGGCCGGCTTCTGAGAAGTCTCAATGAAATGATTGCTCTGTATG
 AGGGTCAATTATGGCAAAGCACGGACATCAATGCCCTTGTTGGGGCGGTGTCAGTGTCTG
 TTCTGATTCTGGCTTGGCAGTAGAAGGTGGCAATAACTGTTGTCAGGGCTCTGC
 AGGCATCAAAAGCAATCTTATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAGACC
 AAGTACACAGGAATCCAACAAAGATGTATGAAGTGGCTACCAAATTGGAACTGAGACTCG
 TTCAAGACTTCTATGACATCGCTTGGCGCACTCGTTGAATCGAAAATGTCGAATATT
 CTTTCTCAACTTGATCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGC
 ACTTTAGTTAAGGGGAATTGAATACATCTATCTTAGCTCTAGACCCATAGATAAATTGG
 CCTTAATACAGTTAACCACTGATAATTCAAGATTGTCATTAACAGTATTGGGATTGTC
 CCTCTGTGAGAGAAAAGGAAGATCTGAGCCATCACAGATGGAACATATGTTGGAGATC
 TTTTCCAAAGAAACTCTTAACTAAAGCACAAATTAAAGCTTTCTGCTCTATGATTATGC
 TGTGAAGAAGCCATGGCTTGCATATCCTCACTATAAGCCCCGGAGAAATGCCCTCTATCA
 TTCTCCATGATGACTTATTACCTCAATGGCATAGAGTGTGCGAGCAAGTGCCTGGAGATG
 AGTGCCATTGAGCCACAACGCTGCACTCCTGCTATCACCGCTGGAACGGCACACAGA
 CATGATTGATCAGGATGGTTATATGAGAACTTAAACTGAACATTGAAGTGCACACTCC
 TTTTCCCTCTAGTCCAAATGACTATCAGTGGCAAAAAAGAACAAAATCTGAGCAGAGA
 TGATTTGAACCAGATATTGCCATTATCATTGTTAAAGTAATCCCTGCTGGTCAT
 AGGAAAAA

FIGURE 26

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLCSCGCPEGAEELRAPPDKIAIIGAGIGGTSAA
YYLRQKFGKDVK
IDLFEREEVGGRLATMVQGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQ
ASGGLLGIYNGE
TLVFEESNWFIIINVIKLVWRYGFQSLRMHMWVEDVLDKFMR
IYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLETI
LQKAGFSEKFNL
EMIA
PVMRVNYGQSTDINA
FVGAVS
LSCSDGLW
AVEGGNKLVC
SGLLQASKSNLISGSV
MYIEEKT
KTKYTG
NPTK
M
YEVVYQIGT
ETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVT
LKV
GELNTS
IFSSR
PIDK
FGLNTVLT
TDNSDLF
I
NSIGIVP
SREKEDP
EP
STDG
TYVW
KIFSQ
ETLT
KAQIL
KLF
LSYD
AVKK
PWL
A
PHYK
P
PEK
CPSI
I
LH
DRL
YY
LNG
IECA
ASAM
EMSA
IAAHNA
ALLAY
HRWNG
HTDM
IDQDG
LYEKL
KTEL

```

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121, 119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

FIGURE 27

CATTTCCAACAAAGAGCACTGGCCAAGTCAGCTCTCTGAGAGAGTCTAGAAGACATGAT
GCTACACTCAGCTTGGGTCTGCCTCTTACTCGTCACAGTTCTCCAACCTTGCCATTG
CAATAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAAACTTATGAAGAAGGTCTTTTATGCTCAAAAAGTAAGAAGCCATTAATGGT
TATTCACTACCTGGAGGATTGTCATAACTCTCAAGCACTAAAGAAAGTATTGCCAAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTCACCTGATGGGCAATATGTGCCTAGAATCATGTTGTAGACCCCTTCTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCACTGAGCTATAA
GAGATGATGGAAAAAGCCTTCACTTCAAAGAAGTCAAATTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTGTAATATTACTATTTAGTTTTTA
ATGTGTTGCAATAGCTTATTAAAATGTTTTAAATCTGA

FIGURE 28

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896
<subunit 1 of 1, 166 aa, 1 stop
<MW: 19171, pI: 8.26, NX(S/T): 1
MMLHSALGLCLLLVTVSSNIAIAIKKEKRPPQTLRGWGDDITWVQTYEEGLFYAQKSKKPL
MVIHHLEDCQYSQALKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLTYEPRDLPILLIENMKKALRLIQSEL
```

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

FIGURE 29

TAAAACAGCTACAATATTCCAGGGCCAGTCACTGCCATTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTGAG**ATG**AAGAAAGTTCTCCTCCTGATCACAGCCATCTGGCA
GTGGCTGTTGGTTTCCAGTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTGTGTTCCCTACCCATATCCATTTCGCCACTTCCAC
CAATTCCATTCCAAGATTCCATGGTTAGACGTAATTTCCTATTCCAATACCTGAATCT
GCCCTACAACCCCCCTCAGCGAAAAG**TAA**ACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTCCTTGAAGAATCAAATTCCGTAAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCATATCTTAGTGTATCTTTA
ATAAACATGAAAGCAAAGATTGGTTCTTAATTCCACA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLITAILAVAVGFPVSDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP
WFRRNFPPIPESAPTTPLPSEK
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

FIGURE 31

FIGURE 32

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pi: 6.36, NX(S/T): 18
MGRGPWAGPSRRLPPLLLLGLARGAAGAPGPDGLDVATCCEHATCQQREGKKICICNYG
FVGNGRTQCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNKTFIGPNDGTFC
DIDECEVSGLCLRGGRCVNTHGSFECYCMGDLPLRNGPEPFHPTTDATSCIEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPKLHCQEINCNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFFSPLVCEKGTWRESTLCTEILTKINDVSLFNDT
CVRWQINSRRNPKISYVISIKGQRLLPMESEVREETVNLTTDSRTPEVCLALYPGTNYTVNI
STAPPRRSMPAVIGFQTAEVLDGDSFNISIFNETCLKLNRSRKVGSEHMYQFTVLGQR
WYLANFSHATSFNFTTREQPVVCLDLYPTTDYTVNTVNLRRSPKRHSVQTIATPPAVQTI
SNISGFNETCLRWSRISKTADMEYMLHIWGQRWYQKEFAQEMTFNISSSSRDPEVCLDLRP
GTNYNVSLRALSELPPVVISLTTQITEPPPLPEVEFFTIVHRGLPLRLRRAKEKNGPISSYQ
VLVLFLALQSTFSCDSEGASSFFSNADADGYVAEELLAKDVDPDAMEPIGDRLYGYEYYN
APLKRGSDYCIILRITSEWNKVRHSCAVWAQVKDSSLMLLQAGVGLGLSLAVVIIITFLSF
SAV

```

Important features of the protein:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126, 146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694, 727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGGAGAGACAGCCAGCAGTTCTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCCTGGGCTGGCTCTGCCCCTTTCTTCTCTGCTGGAGGTTGGGGCTCTGG
 GAGCTCTGCAGGCCAGCACCCGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCACGCCGCTCTGGAAAATCTAAACGCTGAGCCTGAG
 ACCTCTCTAGGGCTCAACCCAGCCGCCATTCCAGAAGCAGAGACCAGGGAGCCAA
 GAGAATTTCCTGCAAGAGAGACCAGGAGTTCAAAAAACATCTCCAACTCATGGTGC
 TGATGCCACCTCGTGGAGACATCAGCCGCAGTGGCAGCCCCAGGGAGCTGGAATGACC
 ACAGTTCAAGACCATCACAGGCAGTGATCCCAGGAAGGCCATTTGACACCCTTGACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCATCCAGTCATC
 ACCCGTCAAGGGCTCAGAGAGCAGCCCTCTCCGACGGCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCCCTCTCCGACGGCCCCATCCAGTCATCACCCGTCAT
 GGTCCCCGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTACTGTCACAAACATCGAG
 GTTATTAAATTGCAAGCATCACAGAAATAGAAACAACAACTTCCAGCATCCCTGGGCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCTCGCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTACAGCCTCTGCCAGACCTGTCC
 ACAGCCGGCACACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCACTCCCCACTAA
 CAGCGCACAGAAAGAGAACTGACAGCACCCGGGCCAGACCCCTCAGTGGAGCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAACCTCAGCCCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGGCAGCTCGGTCTCATAGAGGTGGGTCAAGCAGTGGCAAACAAACTTC
 CTTTGCTGGAGCTGCTCTCTCATAGCCCTCGGAAGCGCCCTCAAGAACACTCACC
 CTTCAGAGACACCGACCATGGACATCGAACCAAGGGCCCTCCCCACAGCAGGGACCC
 CTTCTCTGTCCTCCGACTACAACCAACAGCAGCCAGGGACGAACAGCACCTAGCCAA
 GATCACACCTCAGCGAAGACCAACGATGAAGCCCCAACAGCCACGCCACGACTGCCGGAC
 GAGGCCGACCACAGAC**TGA**GTGCAGGTGAAAATGGAGGTTCTCTCTGCGGTGAGTG
 TGGCTCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGCTGATGCAAGCAGCTCCAC
 CGGGAACTCCACGCCACGCCCTCACTCCAGGTCTCTTACTGCGTGTCAAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGCTCGTATGCCAAAGAGGGTGTGCCCCCTAGCCTG
 GGCCCCCACCGACAGACTGCGACTGCGTTACTGTCAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGCTCAAGCCCTAACCCAGATGTGGCAACAGGACCCCTGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGCTTACCTGTTCCAGAGGTGTGCTGGACTCACCTGG
 CACATGTTCTGTTCACTAAAGAGAGACCTGATCACCCATCTGTGCTTCCATCCTGCA
 TTAAAATCTCAGTGTGGCCAAAAAAA

FIGURE 34

```

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTRKTSFVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAIFDTLCTDDSSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSVTLLAEALVTVTNI
EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVRNPLEETSALSVETPSY
VKVSGAAPVSlEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPPTS
PLPSVPPTTNSSRGTNSTLAKITTSAKTTMKGQQPRPRLPGRGRPQT

```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGCAGTCTGGCAGTGGAGCTCTCCCGGCTGACAGCCACTCCAGAG
 GCC**ATG**CTCGTTCTGCCAGATTGGCTTCAGCTCCTGTTAATTCTGGCTTGGCCA
 GGCAGTCCAATTCAAGAATATGTTCTCCAATTCTGGCTTAGATAAGGGCCTTCAC
 CCCAGAAGTCCAACCTGTGCTTATATCTTGAAGAAAATTTCAGGATCGCGAGGCAGA
 GCGACCACTGGGTCTCCGAGACTTATGCTACGTAAGGAGCTGGCGTCCGCGGGAAATGT
 ACTTCGCTTCTCCCAGACCAAGGTTCTTCTTACCCAAAGAAAATTCCCAAGCTTCC
 CCTGCCTGAGAAGCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
 TTGGCCCAGCTGGGCTGGACTTGGGCCAATTCTTACTATAAACCTGGGACAGAGCTGGA
 ACTGGCTCTGTTCTGGTCAGGAGCCTCATGTTGGGAGACCCACCCCTAACGGAGTA
 AAATGTTGTGTTGCGGTCACTCCATGCCAACAGGTGCTGTTACTTCAACCTGCTGGAT
 GTAGCTAAGGATTGGAATGACAACCCCGGAAAATTCTGGTTATTCTGGAGATACTGGT
 CAAAGAAGATAAGACTCAGGGGTGAATTTCAGCTGAAGAACCTGTGCCAGACTAACGAT
 GCTCCCTCATGCTCCCTGCTGGTGGTGA**CTCTCACCCCTGATCAGTGCCACCCCTCTCGG**
 AAAAGGAGAGCAGCCATCCCTGCCCCAACGTTCTGTAAGAACCTCTGCCACCGTCACCA
 GCTATTCAATTCAACTCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCAAGGGTTCA
 TGGCAAATTACTGCCATGGAGAGTGTCCCTCTCACTGACCATCTCTCAACAGCTCCAAAT
 TATGCTTCTATGCAAGCCCTGATGCGATGCCGTTGACCCAGAGATCCCCAGGCTGTGTAT
 CCCCACCAAGCTGCTCCCATTCCATGCTTACAGGACAATAATGACAATGTCATTCTAC
 GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGGGG**TAGGATGT**CAGAAATGGGAAT
 AGAAGGAGGTGTTCTTAGGGTAAATCTTTAATAAAACTACCTATCTGGTTATGACCACTTA
 GATCGAAATGTC

FIGURE 36

MLRFLPDLAFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVYILKKIFQDREAAA
 TTGVSRDLCYVKELGVGNVLRFPLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQTLI
 AQLGLDLGPNSYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRSPWPQGAVHFNLLDV
 AKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
 RRAAIPVPKLSCKNLCHRQLFINFRDLGWHKWIAPKGFMANYCHGECPFSLTISLNSSNY
 AFMQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

FIGURE 37

CACTTTCTCCCTCTTCCTTACTTTCGAGAAACCGCGTCCCGCTCTGGTCCAGAGAC
 CTCGGAGACCGCGCCGGGAGACGGAGTGCTGGGTGGGGGGACCTGTGGCTCGTA
 CCGCCCCCAACCTCCCTTCTGCACTGCCGTCTCCGGAAGACCTTTCCTCTGTGTT
 TCCCTCACCAGAGTCTGTGATCGCCCGGACTGGCGGAGGAGGAGGCTGGCCGGGGAGA
 TGCTCTAGGGCGGGCGGGAGGAGGCCGGCGGAGCGAACGGCCGGCAGGAAGATGGGC
 TCCCGTGGACAGGGACTTGTGCTGGCTACTGCCGTCTCTGCCTTGCCTCTGGCTGGT
 CCTGAGTCGTGTGCCCATGTCAGGGGAACACAGCAGGAGTGGGAGGGACTGAGGAGCTGC
 CGTCGCCCTCCGGACCATGCGGAGAGGGCTGAAGAACACATGAAAATACAGGGCCAGTCAG
 GACCAAGGGCTCCCTGCTCCCGTCTGGCTCTGTGACCCCGTACCTCATGTACCC
 GGCACCCCGTCCCCAGATCAACATCACTATCTGAAAGGGAGAAGGGTGAACCGGGAG
 ATCGAGGCTCCTAAAGGGAAATATGCCAAACAGCTCAGCAGGGGCCACATCTGGA
 CCCAAAGGGCAGAAGGGCTTACATGGGGCCCCCTGGGAGCGTCAAGAGCCACTACGGCG
 CTTTTCGGTGGCGGAAGAAGCCATGACAGCAACCACTACTACCAAGACGGTGTACTTCG
 ACACGGAGTTCTGTGAAACCTCTACGACCACTTCAACATGTTCACGGCAAGTTCTACTGCTAC
 GTGCCCGCCTACTTCTCAGCCTCAACCGTCAACCTGGAAACAGAGGGACCTACCT
 GCACATCATGAAGAACGAGGAGGAGGGTGTGATCTTGTGCGCAGGTGGCGAACCGAC
 TCATGCAAAGCCAGGCTGATGCTGGAGCTGCGAGAGCAGGACAGGTGTGGTACGCC
 TACAAGGGCGAACGTGAGAACGCCATTCTCAGCGAGGAGCTGGACACCTACCTACCG
 TGGCTACTCTGCTCAAGGCCACCGGGCCTCTCTCTCTCTCTCG
 ACCTTCAACCCCTGCGCTGTGCTGACCCACCGCCCTTCCCGATCCTGGACTCCGACTC
 CCTGGCTTGGCATTCACTGAGACGCCCTGACACACAGAAAGCCAAGCGATCGGTGCTCC
 CAGATCCCGCAGCTCTGGAGAGGAGCTGGCAGATGAAATCACCAGGGGCCACCGC
 GAGAACCTCTGGACCTTCCGGCCCCCTCTGCAACACATCTCAAGTGACCCCGACGGC
 GAGACGGGTGGCGCAGGGCTCCAGGGTGGCACCAGCGGGCTCCAGCTCTGGAAATA
 ATTAGGCAAATCTAAAGGCTCAAAAGGCAAAAGTAAACCTGGAGGACAAAGAAAGGG
 TTGTTATTTTGTCTTTCAGCGCAGGGCTGCTGGCTTCCAAAGAGAGAGGGCTTTCACTGTGAG
 ACTCTGCTTAAGAGAAAGATCAAAGTTAAAGCTCTGGGTCAAGGGAGGGGGGGGGGGAGG
 AAACACTCTGCTTAATCTTTAACCCACGTAGAACTTCTGAGGGATAGGTGGACC
 CTGACATCTCTGTGGCTTCCGGCAAGGGCTCTGTGGTCTTCTGAGTCACAGCTGGAGGT
 GATGGGGCTGGGGCCCCAGGGCTGACCTTCCAGGGGACACTGAGCCCCCTGGCTTGG
 TCCAGGTGGTAGAAGCAGCGGAAGGGCTCTGACAGTGGCAGGGACCCCTGGTCCCCCA
 GGCCTGAGATGTTCTATGAGGGGAGAGCTCTGGTACATCCATGTGGCTCTGCTG
 ACCCTGTGCCAACCCAGACCCCTGGGGGTGGCTTCCATGCTGCCACCTGGCATCGGCT
 TTCTGTGCCGCCCTCCCACAAATCAGCCCCAGAAGGCCGGGGCTTGGCTCTGTTTT
 TATAAAACACCTCAAGCAGCACTGCACTCTCCCATCTCCCTGTGGCTAACGCACCGCTT
 CCACGTGTTGTGTTGGTGGCAGCAAGGGCTGATCCAGACCCCTCTGGCCCACTGCCC
 CATCCAGGCCCTGACCACTGAGCTGAGAGGGCTTTCTAGCTTCAAGAGCAGGGAGAG
 CTGGAAAGGGGCTAGAAAGCTCCGCTTGTCTGTTCTCAGGCTCTGTGAGCCTCACTCCTG
 AGACAGAGTCAAGAGGAAGTACACCTCCAAATCACCCTGTGCAAGGATTACTCTCAGGAGC
 TGGGTGGCAGAGGAGGCAATGCCCCCTGGCAATTGAGGACAGCTGGAGCAGGGTTCG
 GTGTCTCACGGTGTCTCGCCCTGCCATGGCACCCAGACTCTGATCTCCAGGAACCC
 ATAGCCCTCTCCACCTACCCCATGTTGATGCCAGGGCTACTTGTACCCGCTGGCC
 CCCAACCCCCCTGCTCTCTCTCTCCCCCATCCCCACCTGGTTTGACTAATCTGC
 TTCCCTCTCTGGGCTGGCTGGGGATCTGGGTCCCTAAGCTCTCTTAAAGAACTT
 CTGCGGGCTAGACTCTGAAGCGAGTTGCTGTGGCGTGGCCGAAGCAGAGGCCACACTC
 GCTGCTTAAGCTCCCCCAGCTTCCAGAAAACATTAACACTCAGAATTGTGTTTCAA

FIGURE 38

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLAYCLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNNEEVVILFAQVGDRSIMQSQSLMELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCTGGCACGGAGGGAAAGAAGAGAAAAGAAAATCTCCGGGGCTGCTGGGAGCATAAAAGAA
 GCCCTGTGGCCTTGCTGGTTTACCATCCAGACAGACTCAGGCCACAGACGGAC**ATGGCTG**
 CTCAGGGCTGGTCCATGCTCCTGCTGGCTGTCTTAACCTAGGCATCTCGTCCGTCCCTGT
 GACACTCAAGAGCTACCGATGTCGTGTATTCAAGAACACTCTGAATTCACTCTCAAAC
 CATTAAAAATATAATGGTATTCGAGACCATTACTGCAACAGAAAGGAAGTGTAGCAG
 TCCCCAAAATGGGAGTATGATTTGGATCTGATGCTCATGGGTGAAGGCTACTGTT
 GGCCCAATTACTAACAGGTTCCACTGAGGACCTCAAACAAAAGGAATTCCACCGGCAAT
 GAAGCTTCTGTATAGTGTGAGCATGAAAGCCTCTATATCTTCATTGGGAGACCTGAGA
 ACAAGAGAAATATTCCTTCCAATTGGGAGACCTCTAGACACTTGCTGATTAGCTCAC
 AACAGTGATAGGAATTTCATGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**
AAAGCCACTCATGAGGCAAAGAGTTCAAGGAAGCTCCTCTGGAGTTTGGCGTTCTCA
 TTCTTATRACTCTATTCCCGGTTAGCTGGTGTATGGATCTATGAGCTCTTTAAATT
 TATTATAAAATGTTTATTACTAACCTCTAGTGAATGTTCACAGGTGACTGCTCCCCCAT
 CCCCATTCTTGATATTACATATAATGGCATCATACCCCTTATTGACTGACAAACTACT
 CAGATTGCTAACATTGTGCTTAAAGCTTATCCCACTCCACTATGGGCTGTTACAGAG
 TGCATCTCGGTGTAGAGCAAGGCTCCTGCTTCAGTGCCCCAGGGTGAATACTTCTTGAG
 AAAATTTCATTCATCAGAAAATCTGAAATAAAATATGTCTTAATTGAG

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLAVLNLGIFVRPCDTQELRCLCIQEHESEFIPLKLIKNIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

FIGURE 41

CAGACATGGCTCAGTCACTGGCTCTGAGCCTCCTATCCTGGTTCTGGCCTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGCTCAGGACTGTTGCCCAAGTACAGCCAAAGGAAGAT
TCCCAGCCAAGGTTGTCCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCCATCCAG
CTATCCTGTTCTTGGCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAAACCAGGCCAGGG
CTGCAGGAAGGACAGGGGGCCTCCAAGACTGGCAAGAAAGGAAGGGCTCAAAGGCTGCA
AGAGGACTGAGCGGTACAGACCCCTAAAGGGCATAGCCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACCAGCCTCACAGCGCTGAAGCCTGAACCCAAGATGCAAGAAGGGAGGCTATG
CTCAGGGGCCCTGGAGCAGCCACCCATGCTGGCCTTGCACACTCTTCTCTGCTTAAAC
CACCCCATCTGCATTCCAGCTCTACCCCTGCATGGCTGAGCTGCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGGAGAGTCTCCAGGGAGCATGAGAGGGAGGCAGCAGGACTGCCCCCT
TGAAGGAGAATCATCAGGACCCCTGGACCTGATACGGCTCCCCAGTACACCCACCTTCCCT
TGTAAATATGATTATACCTAATGAAATAAAAGCTGTTCTGTCTTCCCNCCA

FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLLLILVLAFGIPRTQGSDDGAQDCCILKYSQRKIPAKVVRSYRKQEPSLGCSIPAI
LFILPRKRSAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDrgASKTGKKKGSKGCKR
TERSQTPKGP

Important features of the protein:

Signal peptide:

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGGAGCAGCCCCAAGCACCAGTGGAGAGGC**ATG**AAGTTACAGTGTGTTCCCTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTT
 CACAGACATGCACCATAAGAGAGTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
 ACACCTTCCCAAATGCACTATCCTGTCACATTGGAGACTCTGCAGATCATTAAGCCCTA
 GATGTGCTGCGTACCAAGAACCTCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
 TCAGGAGCCAACCCCCAAATCTTGAGAAAATCAGCAGCATTGCCAACTCTTCCTCTACA
 TGCAGAAAATCTGCGCAATGTCAGGAACAGAGGAGTGTCACTGCAGGCAGGAAGGCC
 AATGCCACCAGAGTCATCCATGACAACATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCT**TGA**TGACAAGGAACCTGTATAGTGTATCCAGGGATGAACACCCCCCTGTGCGGTTACT
 GTGGGAGACAGCCCACCTTGAAAGGGAGATGGGAAGGCCCTTGCAAGCTGAAACTCC
 CACTGGCTGGCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAGTCTACTGTGTAT
 TTGTAATAAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGAGTAAAGGGCTGCCTT
 CCCATCTAATTATTGTAAGTCATATAGTCCATGTCAGTGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGGTTTCTGAATAATTCCATATTTACCTATGAA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

100002796 - 3115001

FIGURE 45

GCTCCCAGCCAAGAACCTCGGGGCCGCTCGCGGGTGGGAGGAGTTCCCCGAAACCCGGCG
 CTAAGCGAGGCCCTCCCTCCCGCAGATCGAACGCCCTGGGGGGTCAACCCGGCTGGGA
 CAAGAACGCCGCCCTGCTGCCCGGGCCGGGGAGGGGGCTGGGCTGGGCCGGAGGCC
 GGTGTGAGTGGGTGTGCGGGGGGGGGGGCTGGGATGCAATCCGATAAGAAATGCTCGGG
 TGTCCTGGCACCTACCCCTGGGGCCGTAAGGCCCTACTATATAAGGCTGCCGGGGAG
 CCGCCGCCGCGTCAAGACAGGAGCGCTCGCTCAGGATCTAGGCCACGACCATCCAAACCC
 GGCACTCACAGCCCCCGCACGGCATCCGGTGCAGGCCAGCCTCCGACCCCCATGCCGG
 AGCTGCCGGAGAGGCCCAAGGGAGGTGCC**ATGC**GGAGGGTGTGGTGGTCAAGTATGG
 ATCTGGCCGGCTCTGGCTGGCGGGCCGGCCCTCCGCTCTGGACGCCGG
 CCACCTGCACTACGGCTGGGGCACCCATCCGCTGCCACCTGTACACCTCCGGGGCC
 ACGGGCTCTCCAGCTGCTCTCGCAGCTGGGACTGCCGAGCTGGGACTGCCGAG
 CAGAGCCGCACAGCTTGTGAGATCAAGGCAGTCCTCTGCCGACCGTGGCATCAAGGG
 CGTGCACAGCGTGGTACCTCTGCATGGGCGCGACGGCAAGATGCAGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTCAGGGAGAGATCGCCCAAGTGGCTACAATGTGACCGA
 TCCGAGAGACCGCCCTCCGGCTCTCTGCAGCTGCCAACAGCGGAGCTGACAG
 CAGAGGCTTCTCCACTCTCATTTCTGCCTGGCCATGGTCCAGGAGGAGCTG
 AGGACCTCAGGGGCCACTTGGAACTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
 GACCCATTGGCTTGTACCGGACTGGAGGCCGTAGGAGTCCAGCTTGAGAAC**TAAT**
 GAGACCATGCCGGCCCTTCACGTCAGTGCAGGGCTGTGGTACCTGCAGCGTGGGGAGC
 TGCTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
 GTTGACATATTAGAGTTTCCATTGGCAGTGCAGTCTAGGCAATAGACTTGTCTGAT
 CATAACATTGAAAGCTGTAGCTGGCCAGCTGCTGCCCTGGGCCCCCATTCTGCCCTCGA
 GGTTGCTGGACAGCTGCTGCACTGTCAGTTCTGTTGAATACCTCCATCGATGGGAAC
 TCACTCTTTGGAAAAATTCTTATGTCAGCTGAATTCTCATTTCTCATCATT
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAAATTTCAGGAACAGGTGATCCACTCTGA
 AAACAGCAGGTAATTCTACTAACCCCATGTGGAAATTGATCTATCTACTCCAGGG
 ACCATTGCCCCCTCCCAAATCCCTCAGGCCAGAAGTCACTGACTGGAGCAGGCATGCCAAC
 GCTTCAGGAGTAGGGGAAGCTGGAGGCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC
 CTGAGGCCAGTTCTGTCATGGATGCTGCTCTGAGATAACTGCTGTCGGGCTGTCACCTGC
 TTCCATCTCCAGGCCAACAGCCCTGCCCCACCTCACATGCTCCCATGATTGGGCCT
 CCCAGGCCCTCCACCTTATGTCACCTGCACTTCTGTTCAAATCAGGAAAGAGAGAT
 TTGAAGACCCCAAGTCTTGTCATAATTGCTGCTGTTGAGAACAGCAGGGGGAAAGACCTAGAAC
 CCTTCCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTATGATATGTCAG
 TCTCTTATTCTTACATTATTTATGCCCAAATTATATTATGATGTAAGTGAGGTTG
 TTTGTATATTAAGGAGTTGTTGT

FIGURE 46

MRSGCVVVHWILAGLWLA
VAGRPLAFSDAGPHVHYGWGDP
IRLRLHLYTSGPHGLSSCFLR
I RADGVVDCARGQSAHS
LLEIKAVALRTVAIKGVHSV
YRLCMGADGKMQGLQ
YSEEDCAFE
EIRPDGYNV
YRSEKH
RLPVSLSSAK
QRLQYKNRGFL
PLSHFLPML
PMVPEEPEDL
RGHLES
DMFSSPLE
TDSDMPFGL
VTGLEAVR
SPSF
EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 47

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTGTCAGTGGCCTGATGGCG**A**TGGGGACAAA
 GCGCAGTCGAGAGGAAACTGTTGCGCTCTCATATTGGCGATCCCTGTTGCTCCCTGG
 CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
 GTGAAGTTGTCCTGTGCCACTCGGCTTTCTCTCCCCGTGGAGTGGAAAGTTGACCA
 AGGAGACACCACCAAGACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
 TGACCTTCTTGCCAACCTGTTACACCTCAAGTCCTGACACGGGAAGACACTGGGACATAC
 ACTTGTATGGTCTCTGAGGAAGGGCGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
 GCTTGTGCCCTCATCCAAGCCTACAGTTAACATCCCTCCTGCCACCATGGGAACCGGG
 CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
 GGGATAGTGATGCCATCGAACATCCAAAAGCACCCGTGCCCTCAGCAACTCTTCTATGTCCCT
 GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCGTCAAGCCTCTGATACTGGAGAACATACA
 GCTGTGAGGCACCGAATGGTATGGACACCCATGACTTCAAATGCTGTGCGCATGGAGCT
 GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAACCCCTGATCTCCTGGGAAT
 CTTGGTTTTGGCATCTGGTTGCCATAGCCGAGGCCACTTGACAGAACAAAGAACAGGGA
 CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGGCCGAAGTGAAGGAGAACCAAACAG
 ACCTCGTCATTCTGGTG**TGA**GCCTGGCTGGCTACCGCTATCATCTGCATTGCCCTACT
 CAGGTGCTACCGGACTCTGGCCCTGATGTCAGTGTAGTTCACAGGATGCCCTATTTGCTTC
 TACACCCACAGGGCCCTACTTCTCGGATGTTTAATAATGTCAGCTATGTGCCCT
 ATCCTCTCATGCCCTCCCTCCCTTACACTGCTGAGTGGCCTGGAACTTGTAA
 GTGTTTATCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGTATGCCATTGACTCC
 TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAAGGAATCTGCACTCAACTGCCACCTGGC
 TGGCAGGGATCTTGAAATAGGTATCTTGAGCTGGTCTGGCTTTCTGTGACTGAC
 GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGGGCTGAATGGTTGG
 TGATGACACTGGGGCTTCCATCTGGGGCCACTCTTCTGCTTCCATGGGAAGTG
 CCACTGGGATCCCTGCGCTGCTCTGAAATACAAGCTGACTGACATTGACTGTGCTGT
 GGAAAATGGGAGCTCTGTTGAGAGCATAGTAAATTTCAGAGAACCTGAAGGCCAAAG
 GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGCCAGTGCTCACCTG
 TAATCCAGAGGCTGAGGCGAGGCGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA
 ACATGGAGAACCCCTACTGGAAATACAAAGTTAGCCAGGCTGAGTGGTGTGAC
 CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAA

FIGURE 48

MGTKA**QVERKLLCLFI**AILLCSLALGSVTVHSSEPEVRI**PENNPKLSCAYSGFSSPRVEW**
 KFDQGDTTRLV**CYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV**
 KLIVLVPPSKPTVNIPSSATIGNRAV**LTCSEQDGSPPSEYTWFKDGI**VMPTNPKSTRAFSNS
 SYVLNPTT**GELVFDPLSASDTGEYSCEARNGYGT**PMTSNAVRMEAVERNVGVIVAAVLVTLLI
 LLGILVFGIWFAYSRGHFDRTKKGTSSKKV**TIYSQPSARSEG**EFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
 193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 49

CCCCACGCGTCCGAACCTCTCCAGCGATGGAGCCGCCGCTGCTGCCAACCTCACTCTGTGCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTGAGGGACCAGGGGCCATGACC GACCAGCTGAGCAGGGCAGATCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGGCCAGGAAGCGCAACAAAGTTGCAAGCTCATAGTGGAGACGGCACGTTGGCAGCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAGTACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTCGTGTTCAGGAGATCGTGTGGAGAACAACTATACGGCCTTCCAGAACGCCGGCACGAGG GCTGGTTCATGGCTTCAGCGGCAGGGGGGGCCCCCGAGGCTTCCGCAGCGGCCAGAAC CAGCGCGAGGCCACTTCATCAAGGCCCTACCAAGGCCAGCTGCCCTCCCCAACCACGC CGAGAACAGCAAGCAGTTGAGTTGTGGCTCCGCCCCACCGCCGGACCAAGGCACACGGCGGCCAGCCCCACGTCAGTCTGGGGAGGCAGGGGGCAGCAGCCCCCTGGGCCCTCCCAACCCCTTCCCTTAATCCAAGGACTGGCTGGGGTGGCGGGAGGGGAGGCCAGATCCCC GAGGGAGGACCTGAGGGCGCGAAGCATCGAGCCCCAGCTGGAAAGGGCAGGCCGTGCCCCAGGGCGCTGGCACAGTGCCTCCGGACGGGTGGCAGGCCCTGGAGAGGAACACTGAGTGTACCCCTGATCTCAGGCCACCGCCCTGCCCCCTCCAGCCGGCTCTGAAGCC CGCTGAAAGGTAGCGACTGAAAGGCCCTGAGACAAACGCTGGAGGTGGCTGTCTCAAAATCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGCCCCAAACTCTCTGGCTAGACTGTA GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCACCTCTCACATTCCACGACCCAGGCCCTGACCCCCACCCCCAACTCCAGGCCCGGAAATAAACCATTTCTCTGC

FIGURE 50

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTIEIVLE
NNYTAFQNARHEGWFMAFTQGRPRQASRSRQNQREAHFIKRLYQQQLPFPNHAEKQKQFEEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 51

GTTGTGTCTTCAGCAAAACAGTGGATTAAATCTCTTGACACAAGCTTGAGAGCAACACAA
 TCTATCAGGAAAGAAAGAAAAGAAAAACCGAACCTGACAAAAAAGAAGAAAAGAAGAAGA
 AAAAAAATC**ATG**AAAACCATCCAGCCAAAATGCACAATTCTATCTTGGGCAATCTTCAC
 GGGGCTGGCTGCTCTGTCTTCCAAAGGAGTGCCCGTGCAGCGGAGATGCCACCTTCC
 CCAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGGCCACCCCTCAGGTGCACTATT
 GACAACGGGTCACTGGGTTGGCTGGCTGGCTAAACCCAGCACCATCCTCTATGCTGGAAATGA
 CAAGTGGTGCCTGGATCCTCGCTGGCTTCTGAGAACACCCAAACGCAGTACAGCATCG
 AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTAACACCTGCTCGGTGCAGACAGAAC
 CACCCAAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCCAAAATTGTAGAGATTTC
 TTCAGATATCTCCTATTAAATGAAGGAAACAATTAGCCTCACCTGCATAGCAACTGGTAGAC
 CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTGTGAGTGAAGAC
 GAATACTTGGAAATTCAAGGGCATCACCCGGGAGCAGTCAGGGACTACGAGTGCAGTGCCTC
 CAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACATATCACCATA
 TTTCAGAGCCAAGGGTACAGGTGCCCCGTGGACAAAAGGGACACTGCAGTGTGAAGCC
 TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAA
 GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAAACTCATCTTCTCATGCTCTG
 AACATGACTATGGAAACTACATTGCGTGGCCTCAACAGCTGGCCACACCAATGCCAGC
 ATCATGCTATTGGTCCAGGGCGCGTCAGCGAGGTGAGCAACGGCACGTCGAGGGAGGGCAGG
 CTGCGTCTGGCTGCTGCCCTTCTGGCTTGCACCTGCTTCTCAAAATT**TGA**TGTGAGTGC
 ACTTCCCACCCGGAAAGGCTCCGCCACCACCAACACAGCAATGGCAACAC
 CGACAGCAACCAATCAGATATATAAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
 AATTGAGGGAGGGAAACAAAGAATCTTGGGGAAAAGAGTTTAAAAAGAAATTGAA
 AATTGCCCTTGCAAGATATTAGGTACAATGGAGTTCTTTCCAAACGGGAAGAACACAGC
 ACACCCGGCTGGACCCACTGCAAGCTGCATCGTCAACCTTTGGTGCAGTGTGGCA
 GGGCTAGCCTCTGCCACAGAGTGGCCCCACCTGGAAACATTCTGGAGCTGCCATCCCA
 AATTCAATCAGTCCATAGAGACGAACAGAACATGAGACCTCCGGGCAAGCGTGGCGCTGCG
 GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTGAAACGTGAAATAAAAGAGCAAA
 AAAAA

FIGURE 52

MKTIQPKMHNSISWAITFTGLAALCLFQGVPVRSGDATFPKAMDNTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPVVLLSNTQTQYSIEIQNVDVYDEGPYTCCSVQTDNHPK
TSRVHLIVQVSPKIVEISSLSDISINEGNNISLTCIATGRPEPTVWRHISPKAvgFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRRVKVTVNYPYISEAKGTGVPVGQKGTQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

FIGURE 53

GTGGACTCTGAGAACGCCAGGCAGTTGAGGACAGGAGAGAGAACGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGAAGGGAGGACAGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCCTGGTGGAGGAAGACACTCTGGAGAGAGAGAGGGGCTGGGCAGAGATG
 AAGTTCCAGGGGCCCTGGCCTGCCTCTGCTGGCCCTCTGCCTGGCAGTGGGAGGCTGG
 CCCCTGAGACGGAGAGGAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAAGAGGCCGGAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCAAGGGACAGAGAACGAGTTGGCAGTGGAGTCAG
 GCAGGTTCCAGGCTTGGCGAGCAGATGCTTGGCACAGGGCTGGGAAGCAGCCCATG
 CTCTGGGAAACACTGGCAGCAGATTGGCAGACAGGCAGAACAGATGTCATTGCACAGGAGCA
 GATGCTGTCCCGGGCTCTGGCAGGGGGTGCCTGCCACAGTGGCTGGAAACTTCTGG
 AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCTGGAG
 GTCTGGGACTCCGTGGTCCACGGATAACCCGGAAACTCAGCAGGCAGCTTGAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGGCAATGGAGGCCACCAAACCTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGTCCAGCAACTCTGGGGAGGCCAGCGGC
 TCACAGTCGGCAGCAGTGGCAGCAGTGGCAGCAATGGTACAACAAATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGCAGTGGCAGCAGTGGCAGCAGTGG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGCAGGGTACAGCAGCAGTGGCAGTGGCTCTGGGG
 TCCAGCACCGCTCCCTCCGGCAACCACGGTGGAGCAGGGAGGAAATGGACATAAAC
 CGGGTGTGAAAAGCCAGGGATGAAGCCCGGGAGCAGGGAAATCTGGGATTCAAGGGCTTC
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGCCAATGCCCTCTGG
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCGAGCTGGGCAGTGGAGGAGGTGACGCT
 TGGTGGAGTCATAACTGTGAACACTGAGACGTCTCTGGGATGTTAACCTTGACACTTCT
 GGAAGAATTAAATCCAAGCTGGGTTCATCAACTGGGATGCCATAAACAGGACAGAGA
 AGCTCTCGCATCCCGTGACTCCAGACAAGGAGGCCACAGATTGGATGGAGGCCCCACACT
 CCCCTCTAAACACCACCCCTCTCATCACTAACTCTCAGGCCCTGCCCTGAAATAACCTTA
 GCTGCCCAACAA
 AAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, PI: 6.36, NX(S/T): 1

MKFQGPLACLLLALCIGSGEAGPLQSSEESTGTN1GEALGHGLGDALSEGVGKAIGKEAGGA
 AGSKVSEALGCGTREAVGTGVQRQVPGFAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQNPGLGTPWVHGYPGNSAGSFGM
 NPQGAPWGQGGNGGPPNFGINTQGAVAQCPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSSTGSSGSGSNGDNNNGSSGGSSSSGSSSSGSSGGSSGSSGSGSNGGSRGDGSESSW
 GSSTGSSGNHGGGGGNHKGPGCEKPGNEARGSGESGIQGFQQGVSSNMREISKEGNRLL
 GGSGDNYRGQGSSWGGGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKQD
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCAGGTGGCCAGCTCAGCAATGGCAAT
 GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTGGGCTGCGCTCTGCCAGCAGGGTCCC
 AAGCCCTGCAGTGCTACAGCTTGAGCACACCTACTTGGCCCCTTGACCTCAGGGCCATG
 AAGCTGCCAGCATCTCTGTCCATGAGTGCTTGAGGCTATCCTGTCTGGACACCGG
 GTATCGCGCGCCCGTGAACCTGGTGCAGGAAGGGCTGCTGGACCGGGCTCTGCCGGCAGA
 CGCAATCGAACCCGGACGCGCTGCCAGACTACTCGGTGGTGCAGGGCTGCACAACTGAC
 AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCAACCTGAGCCAAGCACCCGACCC
 GCCGACGCTCAGCGGCCGAGTGCTACGCCGTATCGGGGTCCACCAGGATGACTGCCA
 TCGGCAGGTCCCACGAGTCCAGTGTACCAAGGACAGACCGCCCTGCTTCAGGGCAGTGGC
 AGAATGACAGTTGGCAATTCTCAGTCCCTGTATCAGAACCTGCCACCGGGCTCTG
 CACCAACCGAGGGCACCAACCAAGCCCTGGACAGGCCATCGACCTCCAGGGCTCTGCTGTGAGG
 GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTCACCAAGTGCTTCAGCCACCA
 CCCCAGAGCACTACAGGTCCCTGGCCCTGCTCCAGTCCTCTGCTGGTGGGCTCTCAGC
ATAGACCGCCCCCTCAGGATGCTGGGACAGGGCTCACACACCTATTCTGCTGCTTCAGC
 CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 56

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCGTGPAGQTQSNPDALPPDYSVVRGCTTDKCNALMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFASATTPRALLQVLALLPVLLVGLSA
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGGCGCACGCTCCGGCGTCGGCAGGCC
 GCACCTGCAGGTCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCGGCAGGGAGGCC
CATGATTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
 GTGCCCTCGGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCCAACCGGTTGCAG
 GCGGTGGAGGGGGAAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGAGGTGCTTC
 ATCCCAGCCATGGGAGGTGCCCTTGATGTTCTCAAACAGAAAGAAAAGGAGGATC
 AGGTGTTGCTTACATCAATGGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
 ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGTCTCCAGGGAGAAAGACTCTGGCCCTA
 CAGCTGCTCCGTGAATGTCAAGAACAAAGCAGCTTCCAGACTTGTGCAACAGCATCAAAACCT
 TAGAACTCAATGTAATGGTCCCTCAGCTCCATCCTGCCGCTCCAGGGTGTGCCCAT
 GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGGAGTAAGCCCGTGTCCAATACCA
 GTGGGATCGGCAGCTTCCATCCTTCAGACTTCTTGACCCAGCATTAGATGTATCCGTG
 GGTCTTTAACGCTCACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCGAAAGGCCAC
 AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAAGTGAGCACAGGGCTGGAGCTGC
 AGTGGTTGCTGGAGCTTGTGGGTACCCCTGGTGGACTGGGGTTGCTGGCTGGCTGGTCC
 TCTTGATACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCAATGATACTAAGGGAGATGCC
 ATTGCTCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGCC
 TTCCCTGTACCTCCGACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT
 TGACCCCCACGCCAGTCTCCAGGCCAGGGCCCTGCCCTCACCAAGACTGCCACAGAT
 GGGGCCACCCCAACCTCAACCAATATCCCCATCCCTGGGGTTCTCCCTGGCTGAGCCG
 CATGGGTGCTGCGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**
 CCCACCACTATTGGCTAAAGGATTGGGTCTCTCTTCTATAAGGGTCACCTCTAGCAC
 AGAGGCCTGAGTCATGGGAAAGAGTCACACTCTGACCCCTTAGTACTCTGCCACCC
 TTTACTGTGGGAAACCATCTCAGTAAGACCTAAGTGTCCAGGGAGACAGAAGGGAGAAGAGGA
 AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTTATGAAGGCCAGCTG
 CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCAG
 CCCCTGATCTGTACCCACCCCTATCTAACACCAACCTGGCTCCCACTCCAGCTCCCTGT
 ATTGATATAACCTGTCAAGGCTGGCTGGTAGGTTACTGGGGCAGAGGATAGGAATCTC
 TTATTAAAACATGAAATATGTGTTCTTCATTGCAAATTAAATAAGATAACATAA
 TGTTGTATGAAAAA

FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFQKEKEDQVLSYINGVTTSKPGVSLVYSMPSPRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPIRTLWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPPSLSSQALPSPLTTDGAHQPQPIPIPGGVSSGLSR
MGAVPVMVPAQSAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 59

ACTTGCCATCACCTGTGCCCAGTGTGGAAAAATTCTCCCTGTTGAATTGGACATGGAG
 GACAGCAGCAAAGAGGCCAACACAGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
 CATAAGCCCTCAGGACGTCCCCCTAGCTGGAGTTCTGGAACCTCAACAGAACCCCATCCAGT
 CATTITGATTTGCTGTTATTTTTCTTCTTCCACACATTTGATTTTAT
 TTCCGTACTTCAGAA**ATG**GGCCTACAGACCAAAAGTGGCCCAGGGCATGGGCTTTTCCCT
 GAAGTCTGGTTATCATTCCTGGGCTACTCACAGGTGTCAAACTCCTGGCCTGCC
 CTAGTGTGCGCCTGGACAGGAACCTTGTACTGTAATGAGCGGAAGCTTGACCTCAGTG
 CCTCTGGGATCCCGGGCCTAACCGTACTCTACCTCCACAAACAACCAAATTATAATGCTG
 TGGATTCTCAGAACACTGACATGTCAGCTGGTCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCATGAACCTTCCAAGAATGTCAGAGTTCTCCATTGCGAGAAAAC
 AATATTCAACGACATTACGGCTGCTCTGGCCAGCTTGTGAAGAGCTGACACT
 GGATGACAACTTCATATCACACAGTGGGGTGGAAAGCAGGGGCTTCCGGAGGGTATTAGCC
 TCAAATTGTTGTTTGTCTAAGAACCTGAGCAGTGTGCGTGTGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAATTCGAATTGCTGTATATCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGGTCTATTGTGGACGGGAACTCTGACCAACAAGGGTATGCCG
 AGGGCACCTTCAGCCATCTACCAACCTCAAGGAATTTCATATTGACTCTAATTCTGTCC
 CACCCCTCTCCGATCTCCAGGTAGCCATCTGATCAGGCTCTATTGAGGACACCCAGAT
 AAACCAACTTCTTGAGACGGCTTCTCAAAATCTGCTAAAGCTGGAAACGGCTGGATATATCCA
 ACACCAACTTCAGGGATGCTGACTCAAGGGTTTGTGACTGCACTTAAATGGGTACAGAATGGCTCAA
 ATATATCCTTCATCTCAACGTCGGGGHTTCATGTGCGCAAGGTCTGACCAACTCCTGGG
 GGATGGCCGTCAGGGAAATAATATGATCTTGTGCTCTGACCAACTCAGCCTCCACCCCTCTCAT
 CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCACCCCTCTCAT
 TCCAAACCCTAGCAGAACGCTACAGCCCTCAACTCTTACACATCGAAACTTCCACGATT
 CTGACTGGGATGGCAGGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTCATC
 CATTITGTAATGATCTTCATTCAAGTCAGCTGGCTCTCTCTCTCACCGTGATGGCATA
 CAAACTCACATGGGTGAAATGGGCCACAGTTAGGGGGCATGTTAGGGAGCAGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGGGCTGTTAACTAGAGCCCCGATCCACCTATCGGATT
 TGTTAGTGGCACTGGATGTTTAACTACCGCCGGTAGAGACACCATTTGTTAGAGGC
 CACCAACCATGCCCTCATCTGAACACGGCAGCAACACAGCTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGGGCTTGTATGGGGGGCGCGGTGATATT
 GTGCTGGTGGCTTGTCTAGCGTCTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAAATAACACGGGGCCCGCGGAAAGATGATTATTCAGGAGGCAGGACCAAGA
 AGGACAACCTCATCTGGAGATGACAGAAACCAAGTTCTGAGCTCTCTTAAATAACGAT
 CAACCTTAAAGGAGATTTCAGACTGCAAGCCCATTTACACCCCAAATGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
 ACTGCCATACG**TGA**CAGCCAGAGGCCAGCGTTATCAAGGCGACAATTAGACTCTTGAGAA
 CACACTCGTGTGCACTAAAGACACCCAGATTACATTTGATAATGTTACACAGATGCAT
 TTGTGCTTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTTAAAAAAAGTG
 CTATCTTTTATTCAGTTAATACAAACAGTTTGTAACTCTTGTCTTTTAATCTT

FIGURE 60

MGLQTTKWPShGAFFLKS_WLIISLGLYSQVS_KLLACPSVCRCDRN_FVYC_NERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFP_AELHN_VQSVHTVLYGNQLDEFPMNL_PKNVRVL_HLQENNIQ_T
 SRAALAQLL_KLEELH_DDN_SISTVGVEDGA_FREAI_SL_KL_LFLSKN_HLSSV_PVGL_PVLQ_ELR
 VDENRIAVISD_MAFQ_NLTS_LERLIVDGN_LT_NKGIAEGTFS_HL_TK_LKEFSIVR_NSL_HPPPD
 LPGTHL_IR_LY_LQDNQ_INH_IPLTAF_SN_RK_LERL_DISNNQ_LRMLTQGVFD_NLS_NI_KQLT_AR_{NN}
 PWFCDCS_IKWVTEWL_KY_IP_SSLN_RV_GFC_MC_QG_PEV_RGM_AV_RE_LN_MN_LSCPT_TTP_GPL_FPT_P
 APSTASPTTQP_PPTLS_IP_NPS_RS_YTP_PPT_TSK_LPT_IP_DWD_GR_ERV_TPP_IS_ER_IQL_SIHF_VND
 TSIQVSWL_SL_FTV_MAY_KL_TW_VK_MG_HS_LV_GG_IV_QER_IV_SGE_KQ_HL_SL_VN_LE_PR_ST_YR_ICL_VPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQ_TTS_HSM_GSP_FL_LAGL_IGGAV_IF_VL_VVL
 LSVFCWHMHKKGRYTSQ_KW_KY_NR_GR_RK_DDYCEAGT_KK_DN_SILEM_TE_SF_QI_VS_LNND_QLLKG
 DFRLQPIYTPNGGINY_TDC_HIP_{NN}M_RY_CN_SS_VP_DLE_HCH_T

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300, 522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGAACTAAAAGAGTCACCGCAATGAACTGTTATTACTGCTGCCGTT
 TATTTGGGAAATCCTCTCTATGGCCTTGTCTGGAGCAACAGAAAATCTCAAACAAAAGA
 AAGTCAAGCAGGCCAGTGCATCTCATTTGAGAGTGAAAGCGTGGCTGGGTGTGGAAACCAATT
 TTTGTACAGAGGAATGAATACAGACTAGTCATCACATCGGCCAGCTAAAGATCTGATTAGA
 CAATGGAAACAAATTCTTCAGTACAAGCTTGGGAGCTGGAGCTGGAAGTACTTTATCA
 TTGATGAAAGAACAGGTGACATATAITGCCATACAGAAGCTTGTAGAGAGGAGGAGTCCCTC
 TACATCTTAAGAGGCCAGGTAAATGACATCGCTACTGGAAGGGCTGTGGAAACCTGAGTCTGA
 GTTTGTCATCAAAGTTCCGATCTCAATGACAATGAACCAAATTCCTAGATGAACCTTATG
 AGGCCATTGACCCAGAGATGTCCTCCAGAAGGGAACTTGTAGATTCAGGTGACAGCAAGTGT
 GCTGACGATCCCTCAAGTGTAAATATGCTGTCCTCTACAGCTTACTTCAGGCCAGCC
 ATATTTTCTGTGAAACCAACACAGGAGTCATAAGAATATCTCTAAAGATGGAGATGAAAGA
 TCGAAAGATGAGTATTGGGAAATCATTCAGGCAAGGACATGATTGGTCAGCCAGGAGCTG
 TCTGGAAACAACAAAGTGTATTAAATTAAACTTCAGATGTTAATGACAATAAGCTATATTAA
 AGAAAGTTTACCGCTTGTACTGTCCTGTAATCTGACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATTGATGAAATGACATAGGGAGAATGCGAAATGGATTACAGCATTGAAAGAGGAT
 GATTGCCAAACATTGACATTACTAAATCATGAAACTCAAGAAGGAATAGTTATTTAA
 AAAGAAAGTGGATTGGAGCACCAGAACCTACCGTATTAGACCAAAAGTTAAAACCATC
 ATGTTCTGTGAGCAGTCAGAAGTACACACTGGCTTCCACACTTCAATTAGATCCAG
 GTGGAAGATGTTGATGAGCCTCTCTTCTCTTCCCTTCCATATTATGATTGAAAGTTTGA
 AGAAACCCACAGGGATCATTTGTAAGGCGTGGTGTCTGCCACAGACCCAGACAAATAGGA
 ATCTCTATCAGGTTCTTACTTACAGGAGCAACTGGTCAATATCATGAAATGGTAACTC
 ACTAAAGTAACCTACTGGATCTGTAATGCAACTGGTCTGGTACACCTAAAGTATACAGCAC
 AGAAAAATACAATATAGAACAGATCTTCGATCCACTGTATGTCAGTCTTAAACATCA
 ATGATCATGTCCTGAGTTCTCAACTATGAGACTTATGTTGAAAGTGCAGGCTCT
 GGTCAAGGTAATTCAAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGGACCCATT
 TTACTTTAATCTATGTAAGAACACTAAACATTAAGTTTACATGAAATGATGTTGAAAGT
 ATAACACAGCTGTCATTGACTAATAGAAACTGGTTAACCTCAAGAAGAACCTGTCTC
 TACATCTCATCTTAAATGGCAGAACATGGAAATCCGCTCACTTAAAGTACAAAACACCCTTAC
 CATCATGTCCTGACTGTGCACTGGCAGCACAGACCTGCCAGTACCAAGGAGCTT
 TGCTTCCATGGGATTAAGACAGAAGTTATCATTGCTATTCTCATTTGATTATGATCATA
 TTTGGGTTTATTTTGTACTTTGGGTTAAAAGCGGAGAAAACAGATCTTCTGTA
 GAAAAGTGAAGATTGAGAGAATATTTCAATATGATGATGAAAGGGGGTGGAGAAG
 ATACAGAGGCTTGTGATGACAGCTGGAGCTAGGAGTGTACCATATGCGGGAAACGCAAGCT
 CGGAAAACCACAAGCGCTGAGATCAGGAGCTATACAGGAGTCTTGCAGTGGCCCGA
 CAGTGCATATTCAAGGAAATTCTGGAAAAGCTGCAAGGAACCTAAATACTGATCCGTG
 CCCCTCTTTGATTCCCTCCAGACCTACGCTTGTGAGGGAAACAGGGTATTAGCTGGATCC
 CTGAGCTCTTGAATCAGCAGTCTGATCAGGATGAAAGCTGATTACCTTAATGAGTT
 GGGACCTCGCTTAAAGATGAGCTGATGTTGGTCTGCACTGCAAGTCAAATAATTAGG
 GCTTTTACCATCAAATTAAAAGTGTAAATGTTGATGAAACCCATTGAGTTCTGATTCAA
 AGAGTTTGTGCCCTGGCTCATGGGGGAAAGGCCATTGCTATGGAGTTCTGATTCC
 CTGGAGTAATCTCATGGTATTAAAGTCTGAACTGCTCATGCTGATTGAAACAGAGATGTG
 GGGAGAAATGAAACATGCTCACAGGCACTAACACAGGATTTGAGTAAAATG
 TAGGAAAGATATTAAAGTGTAGGAGGACACAGAGTGTAGTCATCTTATGCGATTATAT
 CATTATTACTTAGGAAAGAGTAAAATACCAACAGGAAAATTAAAGGAGCAAAATTG
 CAAGTCAAATGAGTACAAATCGAGATAACATTACATTCTATCATATTGACATGAAA
 ATTGAAAATGATAGTCAGAGAAATTTCATGAAATTATCCATGAGTATTGTTCCCTTAT
 TTTAA

FIGURE 62

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
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IGQLRSLDNNGNNSFQYKLLGAGAGSTFIIDERTGDIYATIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADPSSGNNARL
LYSLLQGPYFSVEPTGVIRISSKMDRELQDEYVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFIKESELYRLTVSEASPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKVDFEHQNHYGIRAKVKNHHVPEQIMKYHTEASTTFIKIQVEDVDEPPLFL
PYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFVNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIIQTISAVDR
DESIEEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIAADNGIP
SLTSTNTLTIHVCDCGDGSQTQTCQYQELVLSMGFKTEVIIAIIICIMIIFGFIFLTGLKQ
RRKQILFPEKSEDFRENIIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSDLQTYAFEGTGSLAGSLSSLESAVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 63

CTT CAG A ACAG GTT CT CCT TCCC AGTC ACC AGT TG CT CG AGT TAG A ATT GT CT GCA **ATGGC**
 CGCC CT GCAG AA AT CT GT GAG CT TT CTT AT GGGG ACC CT GGG C ACC AG CT GC CT C TT C
 TCT TGG CC CT TT GG TA CAG G GAG GAG CAG CT GC G C C AT CAG CT C C ACT G CAG G C TT GAC
 AAG TCC A AT TCC CAG CAG C C T A T A T CACCA ACC CG AC C TT CAT G CT GG C T AAG GAG GAG C T A G
 CTT GG C T G A T A A C A A C A C A G A C G T C G T C T C A T T GGG GAG A A C T G T C C A C G G A G T C A G T A
 T G A G T G A G C G C T G C T A T C T G A T G A A G C A G G T G C T G A A C T T C A C C C T G A A G A A G T G C T G T T C
 C C T C A A T C T G A T A G G T T C C A G C C T T A T A T G C A G G A G G T G G T G C C C T C T G G C C A G G C T C A G
 C A A C A G G C T A A G C A C A T G T C A T A T G A A G G T G A T G A C C T G C A T A T C C A G A G G A A T G T G C A A A
 A G C T G A A G G A C A C A G T G A A A A G C T T G G A G A G T G G G A G A G T C A A A G C A A T T G G G A A C T G
 G A T T T G C T G T T T A T G T C T G A G A A A T G C C T G C A T T **TGA** C C A G A G C A A A G C T G A A A A A T G A A
 T A A C T A A C C C C T T T C C T G C T A G A A A T A A C A A T T G A T G C C C C A A A G C G A T T T T T T T A A C
 C A A A A G G A A G A T G G G A A G C C A A A C T C C A T C A T G A T G G G T G G A T T C C A A A T G A A C C C T G C G T
 T A G T T A C A A A G G A A A C C A T G C C A C T T T G T T T A A G A C C C A G A A G G T G A C T T T C T A A G C A
 T A G A T A T T T A T T G A T A A C A T T C A T T G T A A C T G G T G T T C T A T A C A C A G A A A A C A A T T T A T T T
 T T T A A A T A A T T G T C T T T C C A T A A A A A G A T T A C T T C C A T T C C T T A G G G G A A A A A C C C
 C T A A A T A G C T T C A T G T T C C A T A A T C A G T A C T T T A T T A A A T G T A T T T A T T A T T A T T A T T A
 T A A G A C T G C A T T T A T T T A T A T C A T T T A T T A A T A T G G A T T T A T T A T A G A A A C A T C A T T C G
 A T A T T G C T A C T T G A G T G A A G G C T A A T A T T G A T A T T T A T G A C A A T A A T T A T A G A G C T T A A C
 A T G T T T A T T G A C C T C A A T A A C A C T G G A T A T C C C

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185
><subunit 1 of 1, 179 aa, 1 stop
><MW: 20011, pI: 8.10, NX(S/T): 3
MAALQKSVSSFLMGTATSCLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNNTDVRЛИGEKLFHGVSMSERCYLMQVLNFTLEEVLFQSDRFQPYMQEVVFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 65

GCCCTAACCTCCCAGGGCTCAGCTTTGGAGCTGCCCATTCCTCCGGCTGCAGAAAGGA
 CGCGCCCTCGCTGGCGAAGAAAAGCAAAACTTGTGGGAGGGTTCTGCATCAAC
 CTCCCTCCGAAACCTAACCTCCTGCCGGGGCATCCCTAGACAGAGGAAAGTCTCTGCA
 GAGCCGACCAGCCCTAGTGGATCTGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT
 TTTGAACCCAGTGGAGGCATCGCTGGGCTCGGAAGTCACCGTCCGGCACCAGGTTGG
 CGCTGCCGAGTGGAAACGACAGTTGCGAGCCTCGGCTGCAAGTGGCTCTCTCCCCGG
 GTTGTGTTAGTGTGGCTGAGGCTGAGCTGCGACTTGTGCAAAGTGCAGGAGGCTCAGAGG
 TCCGAAGAGCGCTGCCTCTACTCGCTTCCTCCCTCTCGGTTCCCTACTGTGA
 AATCGAGCGACATTAAACAGGCTCCGGTCTACCGAGACCGATCCGAGCGTTGGCC
 CGGTGTCGCTATTGCATCGGGAGCCCCGAGCACCGCAGA**ATGGCGAGGTTCCGAAGGC**
 CGAACCTGGCCCTGCGAGGTTATGTTACTTGCACCTTCTCACGGGAGCAGTTCTAGTCG
 CCGATGGAAACCCGGAGACAAATCTGTGAGTGGAGTACTCAGGGCTCCCT
 CACACAGAGGAGGGAGTGGAAAGTTGATTACACACGCTACAGGCCACAGGTGGAAAAGAAACTT
 GGACTTCTCAAGCGGTAGACACGCAACCGAGAACGGCTCGGCCAGACTCTCGAGGCCA
 GAAGCTTCACAGACCTGCTGTGGATGATGGGAGGACAATACACTCAGATCGAGGAGGAT
 ACAGACCAAACTATACATATCTCGAATATGGTCATCTGATTCTGCCAGGGGATTT
 ATGGGTGAACATAGACAAATGGAAAGATAAGTGAAGATTATGGAAATATTGTCATAA
 CTCATGCCAACGTCAGACTGAATCTGCTTCGATTTCTGATTTATGGCCACTTCTA
 CGTGAATACACTGTGCAACCGGGGTTTCATATACACTGGAGAAGTCGATCATCGATGCT
 AACAGCCACACAGTACATAGCACCTTAATGGCAATTTCGATCCAGTGTATCCAGAAATT
 CAACACTGTCAGATTGATTAATGGCACAGCACTGTGTCAGTGGGACCATGTACATCTC
 CAGGATAATTATAACCTGGGAAGCTCACCTCCAGCAACCTGTCATGGATGGAGGAAT
 CATCTTGGATACAAAGAAATTCTGCTTGGTCACAGATAAGTCAACCAATCATCCAG
 TGAAAGTGGACTGTCCGATTTGTGCTGTGCTTCCACAGGATCCAACAAATTCCAAATGTT
 CGAAGAAAGACAATTATGATACACCCAGAGTGGACTAACATGTCAAATGTCAAAATACCAAT
 TTGCGCTGGAGATGCCCATTAACCCCATGCTCCAGTTAACAGATGTGGCCCTGTG
 TATCTTCAGATTGGCTCAACTGCAGTTGGTGTAGTAAACTCAAAGATGTCCAGTGG
 TTGATGTCGATCAGGAGACTGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGAT
 GTGTAAGATAACAGAACAGTGGAAACTTCTCTGCCAACACCAACCGTAGGGAGC
 CCACCCAGTCAGGGCTCTAACACACAGAGAGCAGTGACTTCTCAGTTCCACCCAG
 CTCCCTACAGAAGATGATACCAAGATAGCAGTACATCTAAAGATAATGGAGCTTCTACAGA
 TGACAGTGTGAGGAGAAAGGGGAAACCTCCACGCTGGCCTCATCTGGATACCTCA
 TCCTGGTCTCATGGTACGCCAGCATTCTGTGACAGTCTATATGTATCACCACCAACA
 TCAGCAGCCAGCATCTCTTATTGAGAGACCCCAAGCAGATGGCTGCGATGAAGTTAG
 AAGAGGCTCTGGACATCTGCTTATGCTGAAGTTGACCCAGTTGGAGAGAAAAGGGCTT
 TTGATGTCAGAGCAGTGC**TAA**AAATTCTAGGACAGAACACACAGTACTGGTTACAGGTGT
 TAAGACTAAATTTGCTTACCTTAAGACAAACAAACACACACACACAAAGCTC
 TAAGCTGCTGTAGCTGAAGAAGACAGATTCTGGACAAGCTCAGCCAGGAAACAAAGGG
 TAAACAAAAAAACTAAACATTACAGATACCATTTACATGACATAGAATTCCCTAGTGG
 ATGTCATCTAGTCACTGGAAACATCTCCGGTGGACTTATCTGAAGTATGACAAGATTA
 TAATGCTTTGGCTTAGGTCAGGGTTGCAAAGGGATCAGAAAAAAATCATATAAAAGC
 TTTAGTTCATGAGGG

FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVHQAFPHTEEEVEVDSHAYS
 HRWKRNLDLKVADTNRASVGQDSPEPRSFDTLLLDDGQDNNTQIEEDTDHNYYISRIYGPS
 DSASRDLWVNIDQMEKDKVKGILSNTHRQAARVNLSDFDFPFYGHFLREITVATGGFIYTG
 EVVHRLMTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
 LLMDGRIIFGYKEIPVLTQISSTNHVKVGLSDAFVVVHRIQQIPNVRRTIYEYHRVELQ
 MSKITNISAVEMLTPLTCLQFNRCGFCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCP
 EESKEKMCENTEPVETSSRTTTVGATTTQFRVLTTTAAVTSQFPTSLPTEDDTKIALHLK
 DNGASTDDSAEKKGGTLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
 WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
 455-461

FIGURE 67A

GCAGCCCCTAGCAGGG**A**TGGACATGATGCTGTTGGTGCAGGGTCTTGGCTCGAACCAAGTG
 GCTGGCGCGGTGCTCTCAGCTGCTGCTGCTACCCCTGCTCCGGCTGACAGA
 GTGTTGGACTTCCCTGGCGGGCGTGACAAACATGATGGTCAGAAAAGGGGACACGGCGGTG
 CTTAGGTGTTATTGGAAAGATGGAGCTCAAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT
 TTTGGCGGGAGGTGATAACTGGTCACTGGATCTGGAGTTCAATTCAACATTGAATAAAA
 GGGACTACAGCCTCCAGATAACAGAATGTAGATGTGACAGATGATGGCCATACAGTGTCT
 GTTCAGAGCTCAACATACACCCAGAACATGCACTGGCAGTGCTACTGCAAGTCTCTCAA
 GATATATGACATCTCAAATGATGACCGTCATGAAGGAACCAAGTCACTCTACTGTT
 TGGCCACTGGAAACACAGGCTTCCATTCTGGCAGACATCTCCCCATCAGAAAACCA
 TTTGAAATGGACAATTGGACATTATGGAAATTACAAGGGACCAGGGTGGGAATATGA
 ATGCACTGGCGGGAAATGGATGTGTCATCCCGAGATGGAGAAAGTAAAGTTGTTGTCACT
 TTGCTCTCATATTCTAGGAAATTAAATCTGGCACCGTGACCCCCGGACCGAGTGGCCTGATA
 AGATGTGAAGGTGCAGGTGCGCCCTCCAGCCTTGAATGGTACAAAGGAGAGAAGCT
 CTTCAATGGCCAACAAGGAATTATTCTAAATTTAGCACAAAGATCATTCTACTGTTA
 CCAACGTGAGCAGGAGCACTCGGAATTACTGTGTCGGCTGCCAACAAAGCTAGGCACA
 ACCAATGCGAGCCTGCCTTAACCTCCAAGTACAGCCTGAGTGGAAATTACCGGGAGCG
 TGATGTTCTTTCTCTGTCGGTACCTGTGTTGACACTGTCTCTTACACAGCATATTCT
 ACCTGAAGAATGCCATTCTCAA**TAA**ATTCAAAGGCCATAAAAGGCTTTAAGGATTCT
 GAAAGTGTCTGATGGCTGATCCTGGTACAGTTGTTAAAGCAGCCTGGGATATAATC
 AGCAGTGTCTACATGGGGATGATGCCCTCTGTAGAATTGCTCATTATGTAATACTTTAAT
 TCTACTCTTTTGTAGTAGCTACATTACCTGTGAAAGCAGTACACATTGCTCTTTTTAAG
 ACGTGAAGACTGTAATTAGTTAGGGATTAAATTGTGATTTCAGTTGTAATCTAC
 AACATTCTAAAGCATTCACTGCTGCTGAGCTGAGCTGAGTTACAAAAGCAGAA
 TATTGCACTGAAATATGTGATTCTTAAAGGCTGCAATACAAGCATTCAGTCCCCTGTTCAAT
 AAGAGTCATCCACATTTAAAGAGTCATTCTTCTTGTGATAAAAAGGCAATAATA
 TTGCTCTCAGATTATTCTCAAATATAACACATCTAGATTCTGCTCGCATGAT
 TCAGGTTCAAGGAATGAGCCTTGTAAATAACTGGCTGTGAGCTCTGTTCTCTTCTGT
 AAGGTCAGCATGGTGTGCTTCATCAAATAATTCTTCTCTGTCTCCAAATATAAA
 AATGTTGCTAACTTCAATTGAAAGTAAATAAAACAGAGTGTCAAGTTAAACCA
 TACACTATCTAACTGAAACAGGACCTATTGGACTGAAAAACTCTCTGCACTGACAA
 TGGGGTTGAGAATTGTGCCCCACACTAACTCAGTCTGTGATGAGAGACAATTAAAC
 AGTATGAAATATAACATGATTCTTCTGTAGCTAAATGTTAGATCCACCGTGGGA
 AATCATCCCTTAAATGACAGCACGTCACCTCAAAGGATGCTAGCAATACAGCATCT
 TTTCTTCACTAGTCCAAGCCTAAAGTTAAGATGATTGTCAGAAAGGGCACAAGTCC
 TATCACCTAATTACAAGAGTGTGAAAGCCTCATCAATTATTGTTGCGCAGCTAA
 GTTAGTATGACAGGAGCTGCTCTGTGGACAGGGCATTGTCATATTTCACATGAAA
 GTATCACTCAGTTGATGACTGGAATGCTATATATTAAACTCCAAAATATA
 TAACAAACATTCTATAGCTGTTAGTACAGCAGAACATCTCAAATAGCTAATTCTCAATAA
 AATCTTCTATATAGCTTACAGTCAGGAAACAGTAAAGGACATCTTCTTAAAGGAC
 TTCCCTACATGATGATGAAAGATGCGATCAAATAAAGACAAAACACCAAGTGTGAGAATAT
 CTTAAAGATAAGTAAATTATGTGAATGTTAAATTATTCTACTATAAGAACGAA
 AACTACATTGGAAAGGAAAATGCTTACTCTAACATTAACTTACAGGAATAGTTGATGG
 TTTCACTCTTACTAAAGAAGGGCATCACCTGAAAGCCATTACAGGTTGATGAAGTT
 ACCAATTCACTGACACCTAAATTCTACAAATAGTCCCCTTTACAAGTTGTAACACAAAG
 ACCCTATAATAAAATTAGTACAAGAAATTGTGAGTGGTTACATATTGAGATATCTAG
 TATGTTGGCTCTAGCAGGGTGGCTTAAAGCTGTAATTCTTCTCAAGTAAACCTAGT
 CCCAAGTACATCATAAATCAATTAACTGTTAGAAAATGAATCTAAATGAGGGGACATAAG
 TATACTCTTCCACAAATGGCAATAAAGGCAATAAGCTAGTAAATCTACTAATGTAAT
 AAATGTAATGACATTATTGATTGATGACATATTAAAAGGAGTTTGAACAAATGGCATT
 TAACCTTATTATTATTGCTTAAAGAATATTCTTGTGGAAATTGTTGAATAAACTTAA
 AATATTATTGTTGATTGCGACTTAAAGTGGCACACTCCATAATAATCTACTAGAAAT

FIGURE 67B

AGTGGTGCCTACCACAAAAAATGTTAACCATCAGTACCCATTGTTGGGAGAAAGAACAGATC
 AAGAATGCATATTTCAGTGACCCCTTCTAGAGTTAAATACCTCTTGTAAAGGTT
 TGTTAGTAAATTGAGGTATAAACTATGGATGAACCAATAATTAGTTCAAAGTGTGTCATG
 ATTCCAAATTGTTGGAGCTGGTGTTCATCATGTTACCATAGAATGTGACAGAACAGTCAGCT
 CAGTAGCTATATGTTGCCTTATGTTAGAAGAGACTTCTTGAGTGACATTAAATA
 GAGGAGGTATTCACTATGTTCTGTATCACAGCAGATTCTAGTCCTAGGCCCTCGGA
 CAGAGTAAATCATGAGTATTATGTTCAAATAAGGCTACAGTATTGCTT
 TTTTGTGATGTATTGCATATAATGTTCAAGTAGATGTTACATTATGACATATAA
 AAATGTCGATTACCCCATTTTATCACTCCTGACTGTCAGATTGTTCAATTTCAGAATAG
 CAGTTTATAATTGTTATCTTAACTCTATAACAAATTGTTGAGCTGTTCAATTTCAGG
 ANTATATTCTACAAGTCCACTGGGACTCTTGTGCCCCATTTTTTAAAG
 AAGGAAGAAAGAAAAATAAGTACGACTTAAATAAGTGAGAATGGAGAGAAAAGAAAAGAATG
 AAAAGGAAAGGCACTAAAGAGGGAAAAAAAGGAAGGATGGAAGGAATGAGGAAGGAGGG
 AGGAAGGGGAGGAAGGAGAAGAAGGAAGGATGAGGGGAAGGAAGGAATCAGAATATTAGG
 GTAGTTAATCTACACATTGCTTCTAGTTAACCTGCAAGTGGTGTAACTATGTTCAA
 TGATCGCATTGAAACATAAGTCCTTATACCATTAAGTCTTATATGCAAGCAATTATAT
 AATAAAAAGTACTGCCCAAGTTATGTAATGTGGTGTGTTTGAGACACTAAAAGATTGAG
 AGGGAGAATTCAAAACTTAAAGCCACTTTGGGGGTTAAACTTAACTGAAAATTAAATG
 CTTCATCATAACATTAAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG
 GTAAATTCAAGGAAAAAAATATATATATATAAAATACCCCTACATTGAGTCAGAAA
 ACTCTGAAAAGCTGAATTATCAAAGTCATCTATAATGATCAAATTACTGACAATTG
 TTAATTATCATTGCTTAGCTTGTGACACAGCCAAAAGTACCTTATTAATCTTTC
 ATAAAAATTGTTTGAAATCCAGAAATGATTAAAAGAGGTAGGGTTAACTATTAA
 TTGAGATGTGGATGTACAGTATTCAATAGATGAAATGAAATAATGGTATGCCCTAA
 GATTCTTGAATATGTTACTTAAAGACTGGAAAAGCTCTCCGTCTTTAGTAAAAA
 CATCCATATTCTACAACCTGATGTAATAATTGTTGACTGTTCAGGTAATATAAAC
 TCAGTTATCAATTAAAAAAA

FIGURE 68

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>/</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
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EDGASKGAWLNRSSIIFAGGDKWSVDPRSISITLNKRDSLQIQNQVDTDDGPYTCVQVTQH
TPRTMQVHLTVQVPPKIIYDISHNDMTVNEGTVNLTCLATGKPEPSISWRHISPAKPFENGQ
YLDIYGITRDQAGEYECSAENDVSFPDVRKVVVVNFAPTIQEIKSGTVPGRSGLIRCEGA
GVPPPAFEWYKGEEKKLFNGQQGIIIQNFSTRSILTVNTVQEHFGNYTCAANKLGLTNTASL
PLNPPSTAQYGITGSADVLFLSCWYLVLTLSFTSIFYLKNAILQ
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.

amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327

Myelin P0 protein.

amino acids 94-123

FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTCACTCATACATTTACATGGGCACA
 ATTTCACATTCAAGCTCCTATCCTAGGCTAATTATATTATGTTAAATCACTGTTTTG
 TTCTCACGGCTTCCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACCTCTCCAGAAGCA
 AGCGCACATGCCTTCCAAAATAAGAGCAAATTCGCTCTAACACAGGAAAAGACCTGAAGCT
 TTAATTAAAGGGTTACATCCAACCCAGAGCGCTTGTGGGCAGTGGATTGCTCAGCTTCT
 GCGTCACTGCGCGAGGGAAGAGGGAGAGGATCCAGCGTTAGACATGTTATAGACACAAAAA
 CAGCTGGAGATTGGGCTTAAACACCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAAA
 CATTGATTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAACGCTCCAGTCA
 GCCCACAAGATGCCATTGTCCTGGCCCTCTGCTGCTGCTGCTCTCCGGGGCACGGCCAC
 CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCAGACAGCGAGCATATGCAGGAAGCGG
 CAGGAATAAGGAAAAGCAGCCTCCTGACTTCTCGCTTGGTGAGTGGACCTCCAG
 GCCAGTGCCTGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCAGGAAGGCC
 ACCCCCCCAGCAATCCGCGCAGGACAGAACGCCAGGAACCTCTGGAAAGACCT
 TCTCCTCTGCAAATAG

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175
><subunit 1 of 1, 155 aa, 1 stop
><MW: 17194, pI: 10.44, NX(S/T): 0
MYRHKNWRGLKYPSSKEETQVPKTLISGLPGRKSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAGTRKSSLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFFSCK

Important features of the protein:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCCAACCCCCCAGCGTCCGTC**ATG**CCGTGGAGCCTTGGGA
 GCTGGCTGGGTGGCTGCCGTGGTGCAGCATTGGATGGTACCACTCCCGAAAATGTC
 AGAACATGAAATTCTGTTAATTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTGCCAAAGG
 GAACCTGACTTCAACAGCTCAGTACACTAAGTTAGGATATTCCAAGATAAATGCATGAATA
 CTACCTGACGGAATGTGATTCTCAAGTCTTCCAAGTATGGTACCCACACCTTGAGAGTC
 AGGGCTGAATTTCAGATGAGCATTCAAGACTGGTAAACATCACCTCTGTCTGTGGATGA
 CACCATTATTGGACCCCTGGATGCAAGTAGAAAGTACTGCTGATTCTTACATATGCGTT
 TCTTAGCCCCCTAAATTGAGAATGAATACTGAGAACTTGGACTATGAAGAATGTGTATAACTCA
 TGGACTTATAATGTGCAATACTGGAAAACGGTACTGATGAAAAGTTCAAATTACTCCCCA
 GTATGACTTTGAGGTCTCTCAGAAACCTGGAGCCATGGACAACTTATTGTGTTCAAGTTCAG
 GGTTTCTCTGATCGGAACAAAGCTGGGAATGGAGTGAGCTGTGAGCAAACAAACC
 CATGACGAAACGGTCCCCCTCTGGATGGTGCCGTATCCTCATGCCCTCGCTTCTGATGGT
 CTGGCTTGGCACTCCTCGGCTGCTCTCCTGCTGTTACAAGAAGACAAAGTACG
 CCTTCTCCCCTAGGAATTCTCTCCACAGCACCTGAAAGAGTTTGGGCCATCCTCATCAT
 AACACACTTCTGTTTCTCCTTCCATTGTCGGATGAGAATGATGTTTGACAAGCTAAG
 TGTCAATTGAGAAGACTCTGAGAGGGCAAGCAGAATCTGTCAGCTGCAGCCTCGGG
 CCCCGCCCTGGGCAGGGGCCAAAGC**TAGG**CTGAGAAGGAAACACACTCGGCTGGGCACA
 GTGACGTACTCCATCTCACATCTGCCACTGAGGATCAGGGCAGCAAACAGGGCCAAGA
 CCATCTGAGCCAGCCCCACATCTAGAACCTCCAGACCTGGACTTAGCCACCAAGAGAGCTACAT
 TTAAAGGCTGCTTGGCAAAATACTCCATTGGAACTCACTGCCCTATAAAGGCTTCA
 TGATGTTTCAGAACATTGGCACTGAGAGTGTAAATTTCAGCCTTATATCATAAAATAA
 GATCATGTTTAATTGTGAGAACAGGGCCGAGCACAGTGGCTCACGCCGTATAACCAGCA
 CCTTAGAGGTGAGGCAGGGCAGGAGTCACTTGAGGTCAAGGACCGCCTGGCCAATA
 TGGTGAACCCAGTCTACTAAAAACAAAAATTAGCTAGGCATGATGGCGCATGCCAT
 AATCCCAGCTACTCGAGTGCCCTGAGGAGAGATTGCACTGAAACCCGGAGGAGGAGGAGGA
 GGTTGCAGTGAGGCCAGATAGCGGCAGTCAGCCTGCCCTGGTGAACAAAGTGAGACTCCAT
 CTCAAAAAAAAAAAAAATTGTGAGAACAGAACACTTAAATGAGGAATAAGAATGG
 AGATGTTACATCTGGTAGATGTAACATTCTACCAAGATTATGGATGGACTGATCTGAAATCG
 ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTGGATTCTTGC
 GTACTTGAATTATTCTACCTATATGTTTATATGCTGCTGGTGCCTCATTAAAGT
 TTTACTCTGTGTTGC

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGCGLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLFTAQYLSYRIF
QDKCMNTTLCDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKVNVSQYWKNGTDEKFQITPQYDFEVLRNLEPWTT
YCVQVRCFLPDRNKAGEWSEPVCSEQTTHDETVPSSMVAVILMASVFMVCLALLGCFSLWCV
YKKTKYAFSPRNSLQPQHLKEFLGHPHHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPQ
DSCSLGTPPGQGPQS

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristylation sites.

amino acids 6-12, 316-322

FIGURE 73

CGAGCGCCAACCGCTAGCGCTGAATCCGGCTGCTGCCCGCTGCCGCCGCCATGGCCC
 GCGCAGCCCCGCTGCTCGCCCGTTGACCGCGCTCTGCCGCCGCCGCTGGGGAGAT
 GCCCCGGGGCAAATCAGCGGTGGTGGGGCTGGGATTGGGGCTCTGCTGGGCCATT
 TCTCCAGCAGCACTTGGACCTCGGGTGCAGATCAGCTGACGGTACAGAGAAGGGAAACCGTGGGT
 GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGCTGCCCTCCAC
 TCCCTGAGCTGACATGCAGGACTCTGCAAGCTGCTGGGGCTGAGGCACCGCGCAGGGT
 GGTGGCCAGGAGCCCATCTGGCGGGAGCAGCTATGCTGGAGGAGACTGACTGTA
 TGCTGAACCTCTCCGGCTCTGGCACTATGGCATGCTTCTGAGGCTGAGGCTGAGATGTT
 GTGGAGGAGGTATGGAGAAGTCTAGGGATCTATAAGTACCCAGGCCACGGCTATGCC
 CTCGGCTGTGGAGGAGCTGCTCTACTCAGTGGGAGTCCACCTTGTAACTGACCCAGC
 ACTCTGTTGAGCTGAGCTCTGCACTGGCAGTGGCAGCAGCAGCTTATTGATGATGTC
 TCTGCTGCTCTGGCCAGCTATGGCACTGAGCGTACAGCAGCGTGGCCCTTGGAGGAGCAT
 GTCAGTAGCCGGGGCCAAGGCAGCCTGTTGCTGAGGAGGCAATAAGCTGGTTGTT
 CCGGGTGTGAGCTACCAAGGCAATGTTGATCATGGCCACAGTGAACCTCTGTGACCTG
 CACAGCACAGGGAAAGGCCCTGATCAGGCTGGCGTATGAGAATGAGGTAGGAAACAGCTC
 TGACTCTATGACATCTGCTGAGCTGCACTGCCACCCCTGACCTGGACAACAGCAGCAGCAACT
 TAACCTTGCAAGCTTCAACCGCCATTGATGACGTGCAAGGGCTTCCAGGCCACCGC
 GTCTCTTGTCAGGCTACCTCAACTGCTCATCTGGTTTCCCAGACCCCTAAGCTTT
 CCCCTTGCAACATCTTACACAGATTCCCAAGCTTCTCTGCACTCTGGACAACATCT
 GCCCTGCAACATCTGCGAGCTTCCGGGAAAGCAGCCCCAGGGAGGAGCTGTTGGCGA
 GTCCAGTCCCCAAGGCCCTTCTGGGAGCTAAAGACCCCTTCCGTTCTATACTC
 AGTGCAGACAGCTGAGTGGCAGGCCACCCCTCATGGCTCCGGCCACGCTCCGGAGGT
 TTGCACTCATGACCAAGCTTCTACCTCAATGCCCTGGAGTGGCGGCCAGCTCCGGAG
 GTGATGGCGTGGCTGCAAGATGGCCTGCTGGCTTACACCGCTGTAACAGGACCT
 AGAACAGATTGATCAAAGAAGATTGATGACAAGGCTAACAGACTGAGGCTTCTAGG
 GAGAGCCTGGGAACCTTCTACCCCCACTGAAGATGGATCATCCCCAACAGCACCCAGGACTGA
 ATAAGCCATGCTGCCACCAAGGCTTCTTCTGACCCCTCATGTATCAAGCATCTCAGGTG
 ACCTACTGCTGCTATATAAGGGTCCACACGGGGCTGCTGCTTTTTTAAGGGAAA
 GTAAGAAAAGAGAAGGAAATCAAGGCACTATTTTATTTTATTTTTTAAGGGAAA
 AAAAGTTCATCTCACAGGTGCTCAGACTGGTTCTAGCTAGAAACCAAGAACAGACTACG
 GGAGGGAAATATAAGGAGAGAAACTATGAGTCTTATTTTACTGTTTACTACCTACTC
 CCACAACTGACATCAATTGAGGCAACCTAACAGAAATTTACAACCCAGATGTTACAAA
 TAAAGTAGAAGGGAAAGATCAGAAAACCTAACAGAAATGATCATGCTCTGTTACTGTTACT
 TGATGGATTGAGTACCTACTGCAAGACTCCCTAGTCAACCATCTCCAAAGCTGTAACATC
 ACTGCATATTGGAGGGAGATGACTGTTAGGACCAAGGAAGAGATGTCGCTGAATAGTC
 GTCACCATATCTCCAAGCTTCTGGCAACCAAGTGGGGAAAAGAACATGCGAGGCTGAGGAA
 GAGGGAGGCTCTCCTGGCACCTAGAGGAATTAGCCATTCTCTCTTATGCAAAGATTGA
 GGAATGCAACAAATATAAGAAGAGAAACTCCCAAGATGGTAGAGAGCAGTCATCTACCC
 TAGATGTTCATCCAGAGAAGAAGAAGAGGTTGGGGTAGGATTCTCAGAGGTTAGC
 CTGGTACTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAAATTATGCTTCTGCTT
 TTCTACAAACCTTAAAAACTGTTTAAAGAAGAAGTAAAGCCCTTTCATTCAAAA
 AAAAAAA

FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
 ><subunit 1 of 1, 494 aa, 1 stop
 ><MW: 54646, pI: 7.27, NX(S/T): 6
 MARAAPLLAALTALLAAAAGGDAPPGKIAAVVGAGIGGSAVAHFLOQQHFGPRVQIDVYEKGT
 VGGRLATISVNKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVGRSAIFGGEHFMLEETD
 WYLLNNLRLWWHYGIFSLRLQMWWVEVMEKFMRIVKYQAHGYAFSGVEELLYSLGESTFVN
 TQHSVAEPLLQVGVTQRFIDDVSAVLRASYGQSAAMPAFAGAMSLAGAQGSLWSVEGGNKL
 VCSGLLKLTKANVIATVTSVTLHSTEKGKALYQVAYENEVGNSSDFYDIVVIATPLHLDN
 SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYLNSSYFGFPDPKLFPFANILTTDFPSFFC
 NICPVNISASFRRKQPQEAAWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPLYGSRPTL
 PRFALHDQLFYLNALWAASSVEVMAVAAKNVALLAYNRWYQDILKIDQKDLMHKVTEL

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
 237-243, 429-435